

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 01:47:14 ; Search time 77 Seconds
(without alignments)
372.421 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 BACNPIVRGPCIAFFPRWA.....QGNKMKYSEKREYGV 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296	90.0	151	2	P78491 P78491 homo sapien
2	296	90.0	352	1	AMBP_HUMAN P02760 homo sapien
3	272	82.7	337	1	AMBP_PIG P04366 sus scrofa
4	269	81.8	352	1	AMBP_BOVIN P00878 bos taurus
5	264	80.2	125	1	IATR_HORSE P04365 equus caball
6	261	79.3	349	1	AMBP_MOUSE Q025W1
7	261	79.3	349	2	Q925W1 Q925W1 mus musculu
8	261	79.3	349	2	Q9DBJ9 Q9DBJ9 mus musculu
9	259	78.7	346	1	AMBP_MERUN Q62577 meriones un
10	258	78.4	349	1	AMBP_RAT Q64240 rattus norv
11	257	78.1	123	1	IATR_CAPRI P62756 capra hircu
12	257	78.1	123	1	IATR_SHEEP P62757 ovis aries
13	254	77.2	349	1	AMBP_MESAU Q60559 mesocricetu
14	253	76.9	352	2	Q70160 Q70160 cavia porce
15	232	70.5	342	2	Q6P2V8 Q6P2V8 xenopus tro
16	228	69.3	342	2	P70004 P70004 xenopus lae
17	228	69.3	342	2	Q7S246 Q7S246 xenopus lae
18	227	69.0	51	2	P78492 P78492 homo sapien
19	207	62.9	216	2	Q7SXH6 Q7SXH6 brachydanto
20	182	55.3	283	2	Q6ZNI4 Q6ZNI4 homo sapien
21	182	55.3	283	2	Q8TEU8 Q8TEU8 homo sapien
22	182	55.3	576	2	Q6UXZ9 Q6UXZ9 homo sapien
23	176	53.5	571	2	Q7TQW3 Q7TQW3 mus musculu
24	172	52.3	491	2	Q7LDMO Q7LDMO homo sapien
25	172	52.3	548	2	Q6GNZ8 Q6GNZ8 homo sapien
26	169	51.4	759	2	Q8IT91 Q8IT91 ancylostoma
27	165	50.2	107	2	Q8ITQ7 Q8ITQ7 drosophila
28	160	48.6	90	2	Q6T6T5 Q6T6T5 bits gabon
29	159	48.3	2419	2	Q7PEZ1 Q7PEZ1 anopheles g
30	157	47.7	133	2	Q8H245 Q8H245 papio papio
31	156	47.4	35	2	Q951C3 Q951C3 sus scrofa

32	156	47.4	90	2	Q6T6S5 Q6T6S5 bits gabon
33	155	47.1	111	2	Q7M4L3 Q7M4L3 homo sapien
34	155	47.1	523	2	Q14594 Q14594 mus musculu
35	155	47.1	751	2	Q60709 Q60709 mus musculu
36	155	47.1	763	1	APP2_HUMAN Q06481 homo sapien
37	155	47.1	763	2	Q7LUI0 Q7LUI0 homo sapien
38	155	47.1	763	2	Q61482 Q61482 mus musculu
39	155	47.1	765	1	APP2_RAT P15943 rattus norv
40	154	46.8	195	2	Q9DBQ8 Q9DBQ8 mus musculu
41	154	46.8	252	1	SPR2_MOUSE Q9WU03 mus musculu
42	154	46.8	327	2	Q6IND9 Q6IND9 xenopus lae
43	153	46.5	5	1	CSTI_BOVMO P81902 bombyx mori
44	153	46.5	76	2	Q8T7I9 Q8T7I9 bombyx mori
45	152	46.2	122	1	BRIA_BOOMI P83609 boophilus m

ALIGNMENTS

RESULT 1

P78491 PRELIMINARY; PRT; 151 AA.

AC P78491; 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-1-microglobulin (Bikunin) (Fragment).
GN Name=alpha-1-microglobulin-bikunin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91214554; PubMed=1708673;
RA Vetr H., Gebhard W.;
RT "Structure of the human alpha-1-microglobulin-bikunin gene.";
RL Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: X54818; CAN38587.1; -.
DR HSSP: P02760; IBIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot. inh. Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR PROSITE: PR00759; BASICTPASE.
DR PRODOM: PD000222; Prot. inh. Kunz-m; 2.
DR SMART: SM00131; KU; 2. KUNITZ_1; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
FT NON TER 151 151
SQ SEQUENCE 151 AA; 16542 MW; 88F400C5E6CA19831 CRC64;
Query Match 90.0%; Score 296; DB 2; Length 151;
Best Local Similarity 92.7%; Pred. No. 3e-27;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 ACNLPVIRGPCIAFFPRWAVKGCYLFPYGGCGQGNKMKYSEKREYGV 56
DB 85 ACNLPVIRGPCIAFFPRWAVKGCYLFPYGGCGQGNKMKYSEKREYGV 139
AMBP_HUMAN STANDARD; PRT; 352 AA.
ID AMBP_HUMAN P02760; P02759;
AC P02760; P00977; P02759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin (Protein HC)
(Complex-forming glycoprotein heterogeneous in charge) (Alpha-1
microglycoprotein); Inter-alpha-trypsin inhibitor light chain (ITI-LC)
(Bikunin) (HI-30)].
DE Name=AMBP; Synonyms=HCP, ITIL;

RN J. Biol. Chem. 268:8711-8716(1993).
 RP [17]
 RX SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC3.
 RX MEDLINE=91093267; Pubmed=1898735;
 RA Engelild J.J., Salvesen G., Hefta S.A., Thøgersen I.B., Rutherford S.,
 RA Pizzo S.V.;
 RA "Chondroitin 4-sulfate covalently cross-links the chains of the human
 RT blood protein pre-alpha-inhibitor.";
 RT J. Biol. Chem. 266:747-751(1991).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.
 RX MEDLINE=98227321; Pubmed=9566179; DOI=10.1006/jmbi.1997.1582;
 RX Xu Y., Carr P.D., Guss J.M., Ollis D.L.;
 RT Biochim. Biophys. Acta 1482:172-184(2000).
 CC -1 FUNCTION: Alpha-1-microglobulin occurs in many physiological
 CC fluids including plasma, urine, and cerebrospinal fluid. It
 CC appears not only as a free monomer but also in complexes with IGA
 CC and albumin.
 CC -1 FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
 CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
 CC elastase.
 CC -1 SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
 CC one or two heavy chains (H1, H2 or H3) and one light chain,
 CC b1kunit. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
 CC and b1kunit. Inter-alpha-like inhibitor (I-alpha-LI) of H2 and
 CC b1kunit, and pre-alpha-inhibitor (P-alpha-I) of H3 and b1kunit (B)
 CC similarly).
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma
 CC -1 PTM: The precursor is proteolytically processed into two
 CC separately functioning proteins.
 CC -1 PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
 CC chromophores.
 CC -1 PTM: Addition of glycosaminoglycan chondroitin sulfate, allows
 CC cross-linking between the different components.
 CC -1 MISCELLANEOUS: In vitro, the first twelve residues of the amino

Query Match 90.0%; Score 296; DB 1; Length 352;
 Best Local Similarity 92.7%; Pred. No. 6,5e-27;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps

QY 2 ACNLPYVRGCFIAFFPRMAFDVAKGCVLPYVGCGCGNGNKEYSEKREYCGVP 56
 |||||
 DB 286 ACNLPYVRGCFIAFIQMADFADVAKGCVLPYVGCGCGNGNKEYSEKREYCGVP 340

RESULT 3
 AMBP_PIG ID STANDARD; PRT; 337 AA.
 AC P04366; P34954;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMBP protein precursor [containing: Alpha-1-microglobulin; Inter-alpha-
 DE trypsin inhibitor light chain (ITI-LC) (Bikunit) (HI-30) (EI-14)]
 DE (Fragment).
 GN Name:AMBP; Synonyms=ITIL;
 OS Sus scrofa (Pig);
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90353595; Pubmed=1696914; DOI=10.1016/0014-5793(90)81112-2;
 RA Gebhard W., Schreitmüller T., Vetr H., Wachter E., Hochstrasser K.;

RT "Complementary DNA and deduced amino acid sequences of porcine alpha
RT 1-microglobulin and bikunin.",
RL FEBS Lett. 269:32-36(1990).
RN [2]
RP SEQUENCE OF 2-337 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9113723; PubMed=1703444; DOI=10.1016/0167-4781(91)90152-C;
RA Tavakkol A.;
RT "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
RT developmental and tissue-specific expression of two variant messenger
RT ribonucleic acids.",
RL Biochim. Biophys. Acta 1088:47-56(1991).
RN [3]
RP SEQUENCE OF 212-334.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochrassner K., Wechter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor. X. The amino-acid sequences of the
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT inhibitors.",
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -1- FNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with Iga
CC and albumin.
CC -1- FNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase.
CC -1- SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-Li) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PFM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PFM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPR/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X53685; CA37725.1; -;
DR EMBL; X52087; CA36306.1; -;
DR PIR; S11066; TIRGB1.
DR HSSP; P02760; IBIK.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO; GO:0046904; F:calcium oxalate binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0019862; F:IGA binding; ISS.
DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO; GO:0030236; P:anti-inflammatory response; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0042167; P:heme catabolism; ISS.
DR GO; GO:0050777; P:negative regulation of immune response; ISS.
DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO; GO:0007565; P:pregnancy; ISS.
DR InterPro; IPR002968; A1-microglobln.
DR InterPro; IPR011038; Calycin.

DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin_cytoplasmic.
 DR InterPro: IPR002223; Prot_inh_Kunitz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 2.
 DR Pfam: PF00061; Lipocalin_1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00179; LIPOCALIN.
 DR ProDom: PD000222; Prot_inh_Kunitz-m; 2.
 DR SMART: SM00131; Kunitz; 2.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4 By similarity.
 FT CHAIN 5 188 Alpha-1-microglobulin.
 FT CHAIN 191 337 Inter-alpha-tryptsin inhibitor light chain.
 FT DOMAIN 216 266 BPTI/Kunitz inhibitor 1.
 FT BINDING 272 332 BPTI/Kunitz inhibitor 2.
 FT BINDING 38 38 Chromophore (By similarity).
 FT BINDING 96 96 Chromophore (By similarity).
 FT BINDING 122 122 Chromophore (By similarity).
 FT BINDING 134 134 Chromophore (By similarity).
 FT BINDING 134 134 Chromophore (By similarity).
 FT DISULFID 76 173 By similarity.
 FT DISULFID 216 266
 FT DISULFID 225 249
 FT DISULFID 241 262
 FT DISULFID 272 322
 FT DISULFID 281 305
 FT DISULFID 297 318
 FT CARBOHYD 100 100
 FT CARBOHYD 235 235
 FT SITE 226 227 N-linked (GlcNAc...) (potential).
 FT SITE 227 227 Inhibitory (P1) (chymotrypsin, elastase).
 FT SITE 282 283 Inhibitory (P1) (trypsin).
 FT SITE 282 283 T -> M (in Ref. 2).
 FT CONFLICT 49 49 E -> Q (in Ref. 3).
 FT CONFLICT 259 259 E -> S (in Ref. 3).
 FT CONFLICT 270 270 S -> Q (in Ref. 3).
 FT CONFLICT 278 278 G -> A (in Ref. 3).
 FT CONFLICT 283 283 FQ -> IR (in Ref. 3).
 FT CONFLICT 286 286 V -> A (in Ref. 3).
 FT CONFLICT 293 293 Q -> K (in Ref. 3).
 FT CONFLICT 311 311 E -> Q (in Ref. 3).
 FT CONFLICT 315 315
 SQ SEQUENCE 337 AA; 37690 MW; 1F630FF98E3CD70F CRC64;

Query Match 82.7%; Score 272; DB 1; Length 337;
 Best Local Similarity 82.1%; Pred. No. 4.4e-24;
 Matches 46; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTAFPPRAFAVKGKCTLPFGGCGGNGKFKYSKEKREYCGVP 56
 DB 270 EACSLPIVSGPGRGFQIWAFAVQKCYLFTNYGCGGNGNPFYSKECKEYCGVP 325

RESULT 4
 AMBP_BOVIN STANDARD; PRT; 352 AA.
 ID AMBP_BOVIN STANDARD; PRT; 352 AA.
 AC P00978; P35420; Q28020;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMBP protein precursor [contains: Alpha-1-microglobulin; Inter-alpha-tryptsin inhibitor light chain (ITI-IC) (Bikunin) (H1-30) (BI-14) (Cumulus extracellular matrix stabilizing factor) (ESF)].
 GN Name=AMBP; Synonyms=ITIL;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96201710; PubMed=8611630; DOI=10.1016/0167-4781(95)00235-9;
 RA Lindqvist A., Aakerstrom B.,
 RT "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization
 of liver cDNA and urinary alpha 1-microglobulin.",
 RL Biochim. Biophys. Acta 1306:98-106(1996).
 RN [12]
 RP SEQUENCE OF 227-349.
 RX MEDLINE=85225967; PubMed=2408637;
 RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.,
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 the inter-alpha-tryptsin inhibitor. X. The amino-acid sequences of the
 trypsin-released inhibitors from horse and pig inter-alpha-tryptsin
 inhibitors.",
 RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 RN [13]
 RP SEQUENCE OF 227-348.
 RX MEDLINE=84133807; PubMed=6199275;
 RA Hochstrasser K., Wachter E.,
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 the inter-alpha-tryptsin inhibitor. VII. Determination of the amino-
 acid sequence of the trypsin-released inhibitor from bovine inter-
 alpha-tryptsin inhibitor.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
 RN [14]
 RP SEQUENCE OF 206-219.
 RC TISSUE=Fetal serum;
 RX MEDLINE=92291130; PubMed=1376324;
 RA Chen L., Mao S.J.T., Larsen W.J.,
 RT "Identification of a factor in fetal bovine serum that stabilizes the
 cumulus extracellular matrix. A role for a member of the inter-alpha-
 trypsin inhibitor family.",
 RL J. Biol. Chem. 267:12380-12386(1992).
 RN [15]
 RP REACTIVE SITES.
 RX MEDLINE=84133808; PubMed=6199276;
 RA Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.,
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 the inter-alpha-tryptsin inhibitor. VII. Characterization of the bovine
 inhibitor as double-headed trypsin-elastase inhibitor.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
 CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
 fluids including plasma, urine, and cerebrospinal fluid. It
 appears not only as a free monomer but also in complexes with IgA
 and albumin.
 CC -1- FUNCTION: Inter-alpha-tryptsin inhibitor, present in plasma and
 urine, inhibits trypsin, plasmin, and lysosomal granulocytic
 elastase.
 CC -1- FUNCTION: May diffuse into follicular fluid after an ovulatory
 stimulus to act as structural linker that ensure normal cumulus
 expansion, through stabilization of the cumulus extracellular
 matrix thus supporting the process of ovulation.
 CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
 one or two heavy chains (H1, H2 or H3) and one light chain,
 bikunin. Inter-alpha-inhibitor (I-alpha-1) is composed of H1, H2
 and bikunin, inter-alpha-like inhibitor (I-alpha-1i) of H2 and
 bikunin, and pre-alpha-inhibitor (P-alpha-1) of H3 and bikunin (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PTM: The precursor is proteolytically processed into two
 separately functioning proteins.
 CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
 chromophores (By similarity).
 CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
 family.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL, U35642; AAB07599.1; -.
 DR PIR, S68149; TIBOBI.
 DR HSSP, P02760; IBIK.
 DR GO, GO:0005576; C:extracellular; ISS.
 DR GO, GO:0005886; C:plasma membrane; ISS.
 DR GO, GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO, GO:0046904; F:calcium oxalate binding; ISS.
 DR GO, GO:0020037; F:heme binding; ISS.
 DR GO, GO:0019862; F:IgA binding; ISS.
 DR GO, GO:0030568; F:protein homodimerization activity; ISS.
 DR GO, GO:0042803; F:protein inhibitor activity; ISS.
 DR GO, GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO, GO:0030236; F:anti-inflammatory response; ISS.
 DR GO, GO:0007155; P:cell adhesion; ISS.
 DR GO, GO:0042167; P:heme catabolism; ISS.
 DR GO, GO:0050777; P:negative regulation of immune response; ISS.
 DR GO, GO:0046329; P:negative regulation of JNK cascade; ISS.
 DR GO, GO:0007565; P:pregnancy; ISS.
 DR InterPro, IPR002968; A1-microglobulin.
 DR InterPro, IPR011038; Calycin.
 DR InterPro, IPR002345; Lipocalin.
 DR InterPro, IPR00566; Lipocalin cytochrome P-450.
 DR InterPro, IPR002223; Prot. Inh. Kunz-m.
 DR Pfam, PF00014; Kunitz BPTI; 2.
 DR Pfam, PF00061; Lipocalin; 1.
 DR PRINTS, PR00759; BASICPTASE.
 DR PRINTS, PR00179; LIPOCALIN.
 DR ProDom, PD000222; Prot. Inh. Kunz-m; 2.
 DR SMART, SM00131; KU; 2. _Inh_Kunz-m; 2.
 DR PROSITE, PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE, PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE, PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 203 Alpha-1-microglobulin.
 FT CHAIN 206 352 Inter-alpha-trypsin inhibitor light chain.
 FT DOMAIN 231 281 BPTI/Kunitz inhibitor 1.
 FT BINDING 287 337 BPTI/Kunitz inhibitor 2.
 FT BINDING 53 53 Chromophore (By similarity).
 FT BINDING 111 111 Chromophore (By similarity).
 FT BINDING 137 137 Chromophore (By similarity).
 FT BINDING 149 149 Chromophore (By similarity).
 FT DISULFID 91 188 By similarity.
 FT DISULFID 231 281 By similarity.
 FT DISULFID 240 264 By similarity.
 FT DISULFID 256 277 By similarity.
 FT DISULFID 287 337 By similarity.
 FT DISULFID 296 320 By similarity.
 FT DISULFID 312 333 By similarity.
 FT SITE 241 242 Inhibitory (PI) (chymotrypsin, elastase).
 FT SITE 297 298 Inhibitory (PI) (trypsin).
 FT CARBOHYD 115 115 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 223 223 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 250 250 N-linked (GlcNAc...) (potential).
 FT CONFLICT 209 209 T -> G (in Ref. 4).
 FT CONFLICT 217 217 A -> D (in Ref. 4).
 FT CONFLICT 268 268 G -> L (in Ref. 2 and 3).
 FT CONFLICT 274 274 E -> Q (in Ref. 2 and 3).
 FT CONFLICT 298 299 SY -> AF (in Ref. 2 and 3).
 FT CONFLICT 330 330 E -> Q (in Ref. 2 and 3).
 FT CONFLICT 346 346 E -> R (in Ref. 2 and 3).
 FT SEQUENCE 352 AA; 39235 MW; EDJ1CSA02E70B19 CRC64;

Query Match 81.8%; Score 269; DB 1; Length 352;
 Best Local Similarity 78.6%; Pred. No. 1e-23;
 Matches 44; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Oy 1 EACNLPVIRGPCIAFPFMAPDAVKGCVLPFGGCGQNGNKFYSKECREYCGVP 56
 Db 285 EACNLPVIRGPCIAFPFMAPDAVKGCVLPFGGCGQNGNKFYSKECREYCGVP 340

RESULT 5
 IATR_HORSE STANDARD; PRT; 125 AA.
 AC P04375.
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (Irt) (HI-14) (Inhibitory
 DE fragment of Irt) (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE OF 3-125.
 RX MEDLINE=8525967; PubMed=2408637;
 RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
 RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
 RT inhibitors";
 RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 RN [2]
 RP SEQUENCE OF 1-31.
 RC TISSUE=urine;
 RX PubMed=1627153;
 RA Veerargavan K., Singh K., Wachter E., Hochstrasser K.;
 RT "Characterization of a trypsin inhibitor from equine urine";
 RL Biochem. Int. 26:405-413(1992).
 CC -1- FUNCTION: This inhibitory fragment, released from native Irt after
 CC limited proteolysis with trypsin, contains two homologous domains.
 CC Whereas the second domain is a strong inhibitor of trypsin, the
 CC first domain interacts weakly with PMN-granulocytic elastase and
 CC not at all with pancreatic elastase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: The amino acid at position p2' (17) appears to
 CC determine the specificity of the inhibition of domain 1.
 CC Inhibitors with methionine in this position interact weakly with
 CC chymotrypsin and elastase; those with leucine interact strongly.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR PIR, A01210; TIBOBI.
 DR HSSP, P02760; IBIK.
 DR InterPro, IPR002223; Prot. Inh. Kunz-m.
 DR Pfam, PF00014; Kunitz BPTI; 2.
 DR PRINTS, PR00759; BASICPTASE.
 DR ProDom, PD000222; Prot. Inh. Kunz-m; 2.
 DR SMART, SM00131; KU; 2.
 DR PROSITE, PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE, PS00279; BPTI_KUNITZ_2; 2.
 KW Direct protein sequencing; Glycoprotein; Plasma; Repeat;
 KW Serine protease inhibitor.
 FT NON TER 1 1
 FT DOMAIN 7 57 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 63 113 BPTI/Kunitz inhibitor 2.
 FT SITE 17 18 Reactive bond for chymotrypsin and
 FT SITE 17 18 elastase.
 FT SITE 73 74 Reactive bond for trypsin.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT DISULFID 63 113
 FT DISULFID 72 96
 FT DISULFID 88 109
 FT CARBOHYD 25 26
 FT CONFLICT 13 13 N-linked (GlcNAc...)
 FT CONFLICT 13 13 Q -> E (in Ref. 2).
 FT NON TER 125 125
 FT SEQUENCE 125 AA; 13725 MW; CE79B4D801DE42D5 CRC64;


```

RESULT 7
0925W1 PRELIMINARY; PRT; 349 AA.
ID 0925W1
AC 0925W1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Alpha-1-microglobulin/bikunin precursor (BMEhl.2.1) (Alpha 1
microglobulin/bikunin, variant 1).
GN Name=Abmp; Synonym=AMBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99326507; PubMed=10395906; DOI=10.1016/S0378-1119(99)00191-2;
RA Lindqvist A., Rouet P., Sallier J.P., Akerstrom B.;
RT "The alpha-1-microglobulin/bikunin gene: characterization in mouse and
evolution.";
RL Gene 234:329-336(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Collins E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rabe S.S., Loughlan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosh S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -1- SIMILARITY: Contains 2 BPT1/Kunitz inhibitor domains.
DR EMBL, AF034692; AAD01995.1; -.
DR EMBL, BC021660; AAH21660.1; -.
DR EMBL, AL691496; CAD83043.1; -.
DR HSSP, P02760, 1BIK.
DR MGD, MGI:88002, Abmp.
DR GO, GO:0005615, C:extracellular space, TAS.
DR GO, GO:0005865, C:plasma membrane, ISS.
DR GO, GO:0019855, F:calcium channel inhibitor activity, ISS.
DR GO, GO:0046904, F:calcium oxalate binding, ISS.
DR GO, GO:0020037, F:heme binding, ISS.
DR GO, GO:0019862, F:IGA binding, ISS.
DR GO, GO:0030568, F:plasmin inhibitor activity, ISS.
DR GO, GO:0048033, F:protease inhibitor activity, ISS.
DR GO, GO:0030304, F:trypsin inhibitor activity, ISS.

```

```

DR GO, GO:0030236, P:anti-inflammatory response, ISS.
DR GO, GO:0007155, P:cell adhesion, ISS.
DR GO, GO:0042167, P:heme catabolism, ISS.
DR GO, GO:0050777, P:negative regulation of immune response, ISS.
DR GO, GO:0046329, P:negative regulation of JNK cascade, ISS.
DR GO, GO:0007565, P:pregnancy, ISS.
DR Pfam, PF00014, Kunitz_BPT1, 2.
DR Pfam, PF00061, Lipocalin, 1.
DR PRINTS, PR01215, A1MCGLOBULIN.
DR PRINTS, PR00759, BASICPTASE.
DR PRINTS, PR00179, LIPOCALIN.
DR ProDom, PD000222, Prot_Inh_Kunz-m, 2.
DR SMART, SM00131, KU, 2.
DR PROSITE, PS00280, BPT1_KUNITZ_1; 2.
DR PROSITE, PS00279, BPT1_KUNITZ_2; 2.
DR PROSITE, PS00213, LIPOCALIN; UNKNOWN_1.
DR LIPOCALIN, Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 349 alpha-1-microglobulin/bikunin.
SQ SEQUENCE 349 AA; 39029 MW; CFB9208D37DF0021 CRC64;
Query Match 79.3%; Score 261; DB 2; Length 349;
Best Local Similarity 78.2%; Pred. No. 9.2e-23;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
OY 2 ACNLPYVRGPCIAPFPBPAVVKGCYLFPYGGCGGNGNRPYSKCEGECYGV 56
DB 285 ACNLPYVRGPCIAPFPBPAVVKGCYLFPYGGCGGNGNRPYSKCEGECYGV 339
RESULT 8
09DBJ9 PRELIMINARY; PRT; 349 AA.
ID 09DBJ9
AC 09DBJ9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300004018 product:alpha 1 microglobulin/bikunin, full
insert sequence.
DE insert sequence.
GN Name=Abmp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

```

RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Kikunishi T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Kasukawa T., Kato H.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:11757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Furumichi Y., Furuno M.,
 RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Koda M., Koya S., Kuzuhara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka M.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the lipocalin family.
 CC -1- SIMILARITY: Contains 2 BPT/Kunitz inhibitor domains.
 DR EMBL: AK004907; BMB23659.1; -.
 DR HSSP: P02760; IBIK.
 DR MGD: MGI:88002; Ambp.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0005865; C:plasma membrane; ISS.
 DR GO: GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO: GO:0046904; F:calcium oxalate binding; ISS.
 DR GO: GO:0020037; F:heme binding; ISS.
 DR GO: GO:0019862; F:iga binding; ISS.
 DR GO: GO:0030568; F:plasmin inhibitor activity; ISS.
 DR GO: GO:004803; F:protein homodimerization activity; ISS.
 DR GO: GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO: GO:0030236; F:anti-inflammatory response; ISS.
 DR GO: GO:0007155; P:cell adhesion; ISS.
 DR GO: GO:0042167; P:heme catabolism; ISS.
 DR GO: GO:0050777; P:negative regulation of immune response; ISS.
 DR GO: GO:0046329; P:negative regulation of JNK cascade; ISS.
 DR GO: GO:0007565; P:pregnancy; ISS.
 DR InterPro: IPR002968; A1-microglobln.
 DR InterPro: IPR011038; Calycin.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin cyfABP.
 DR InterPro: IPR002223; Prot inh_kunz-m.
 DR Pfam: PF00014; Kunitz_BPT1_2.
 DR Pfam: PF00061; Lipocalin_1.
 DR PRINTS: PR01215; A1MCGLOBULIN.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Prot inh_kunz-m; 2.
 DR SMART: SM00131; KU_2.
 DR PROSITE: PS00280; BPT1_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPT1_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
 KW Lipocalin.
 SQ SEQUENCE 349 AA; 39101 MW; E593222FBC01BC3D CRC64;

Query Match 79.3%; Score 261; DB 2; Length 349;
 Best Local Similarity 78.2%; Pred. No. 9; ze-23;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPVAGPCIAFPFWAPDAVKGKCYLPFYGGCGGNGNKFYSKECREYCGVP 56
 DB 285 ACNLPVAGPCIAFPFWAPDAVKGKCYLPFYGGCGGNGNKFYSKECREYCGVP 339
 RESULT 9
 AMBP_MERUN STANDARD; PRT; 346 AA.
 ID AMBP_MERUN 062577; 062576;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
 DE trypsin inhibitor light chain (Irr-LC) (Bikunin) (HI-30)].
 GN Name=AMBP; Synonyms=ITLI;
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OX NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95110820; PubMed=7529051; DOI=10.1016/0167-4638(94)90198-8;
 RA Ide H., Itoh H., Nawa Y.,
 RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
 RT Mongolian gerbil and Syrian golden hamster in comparison with man and
 RT other species."
 RL Biochim. Biophys. Acta 1209:286-292(1994).
 CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
 CC fluids including plasma, urine, and cerebrospinal fluid. It
 CC appears not only as a free monomer but also in complexes with IGA
 CC and albumin (By similarity).
 CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
 CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
 CC elastase (By similarity).
 CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
 CC one or two heavy chains (H1, H2 or H3) and one light chain,
 CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
 CC and bikunin, inter-alpha-like inhibitor (I-alpha-II) of H2 and
 CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PTM: The precursor is proteolytically processed into two
 CC separately functioning proteins.
 CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
 CC chromophores (By similarity).
 CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
 CC family.
 CC -1- SIMILARITY: Contains 2 BPT/Kunitz inhibitor domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D31813; BAA0600.1; -.
 DR HSSP: P02760; IBIK.
 DR GO: GO:0005576; C:extracellular; ISS.
 DR GO: GO:0005865; C:plasma membrane; ISS.
 DR GO: GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO: GO:0046904; F:calcium oxalate binding; ISS.
 DR GO: GO:0020037; F:heme binding; ISS.
 DR GO: GO:0019862; F:iga binding; ISS.
 DR GO: GO:0030568; F:plasmin inhibitor activity; ISS.
 DR GO: GO:0042803; F:protein homodimerization activity; ISS.
 DR GO: GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO: GO:0030236; F:anti-inflammatory response; ISS.

```

DR GO:0007155; P:cell adhesion; ISS.
DR GO:0042167; P:heme catabolism; ISS.
DR GO:0050777; P:negative regulation of immune response; ISS.
DR GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO:0007565; P:pregnancy; ISS.
DR InterPro: IPR002968; A1-microglobulin.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin cytochrome P-450.
DR InterPro: IPR002223; Prot. Inh. Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00179; LIPOCALIN.
DR ProDom: PD000222; Prot. Inh. Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
KW Glycoprotein; Lipocalin; Plasma; Repeat; Serine protease inhibitor;
KW Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 346 Inter-alpha-trypsin inhibitor light
FT CHAIN 205 346 Chain.
FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
FT DOMAIN 286 336 BPTI/Kunitz inhibitor 2.
FT BINDING 52 52 Chromophore (By similarity).
FT BINDING 110 110 Chromophore (By similarity).
FT BINDING 136 136 Chromophore (By similarity).
FT BINDING 148 148 Chromophore (By similarity).
FT DISULFID 90 187 By similarity.
FT DISULFID 230 280 By similarity.
FT DISULFID 239 263 By similarity.
FT DISULFID 255 276 By similarity.
FT DISULFID 286 336 By similarity.
FT DISULFID 295 319 By similarity.
FT DISULFID 311 332 By similarity.
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).
FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase)
FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase)
FT SITE 296 297 Inhibitory (PI) (trypsin) (By
FT SITE 296 297 similarity).
SQ SEQUENCE 346 AA; 38643 MW; F1A463810918D5F CRC64;
Query Match 78.7%; Score 259; DB 1; Length 346;
Best Local Similarity 76.4%; Pred. No. 1.6e-22;
Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
OY 2 ACNLEPIVGPCTIAFPFPAFAVKGKCVLPFYGGCGGNGNKFYSKEGREGVGP 56
DB 285 ACNLEPIVGPCTIAFPFPAFAVKGKCVLPFYGGCGGNGNKFYSKEGREGVGP 339

```

```

RT "Rat alpha 1-microglobulin: co-expression in liver with the light
RT chain of inter-alpha-trypsin inhibitor.";
RT Biochim. Biophys. Acta 1130:63-67(1992).
RN [2]
RP SEQUENCE OF 141-195 FROM N.A.
RX MEDLINE=87033744; PubMed=242963;
RA Kastern W., Björck L., Aakerström B.;
RT "Developmental and tissue-specific expression of alpha 1-microglobulin
RT mRNA in the rat.";
RL J. Biol. Chem. 261:15070-15074(1986).
RN [3]
RP SEQUENCE OF 283-343, AND CHARACTERIZATION.
RC STRAIN=Miscar;
RX MEDLINE=89053978; PubMed=326366;
RA Kido H., Yokogoshi Y., Katunuma N.;
RT "Kunitz-type protease inhibitor found in rat mast cells. Purification,
RT properties, and amino acid sequence.";
RL J. Biol. Chem. 263:18104-18107(1988).
RN [4]
RP PROCESSING.
RX MEDLINE=9414892; PubMed=7508921;
RA Itoh H., Ide H., Ishikawa N., Nawa Y.;
RT "Mast cell protease inhibitor, trypstatin, is a fragment of inter-
RT alpha-trypsin inhibitor light chain.";
RL J. Biol. Chem. 269:3818-3822(1994).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with IgA
CC and albumin (By similarity).
CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase (By similarity).
CC -1- FUNCTION: Trypsin is a trypsin inhibitor. It inhibits blood
CC coagulation factor Xa and trypsin about 100-fold more rapidly
CC than porcine pancreatic trypsin and chymase. It is a monomer but
CC is also found in mast cells as a complex with trypsin.
CC -1- SUBUNIT: 1-alpha-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC b1kunitz, inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and b1kunitz, inter-alpha-like inhibitor (I-alpha-LI) of H2 and
CC b1kunitz, and pre-alpha-inhibitor (P-alpha-I) of H3 and b1kunitz (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized in the liver and secreted in
CC plasma. Trypsin is present in mast cell granules.
CC -1- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -1- PTM: Heavy chains are interlinked with b1kunitz via a chondroitin
CC 4-sulfate bridge to the their C-terminal aspartate (By
CC similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S87544; AAB21782.1; -.
DR EMBL: J02600; AAA41596.1; -.
DR PIR: S21089; S21089.
DR HSSP: P02760; 1BTK.
DR RGD: 2102; Ambp.
DR GO:0005576; C:extracellular; ISS.
DR GO:0005886; C:plasma membrane; ISS.
DR GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO:0046904; F:calcium oxalate binding; ISS.

```

DR GO; GO:0020037; F-heme binding; ISS.
 DR GO; GO:0019862; F-iga binding; ISS.
 DR GO; GO:0030568; F-plasmin inhibitor activity; ISS.
 DR GO; GO:0042803; F-protein homodimerization activity; ISS.
 DR GO; GO:0030304; F-trypsin inhibitor activity; ISS.
 DR GO; GO:0030236; Plant-inflamatory response; ISS.
 DR GO; GO:0071555; P-cell adhesion; ISS.
 DR GO; GO:0042167; P-heme catabolism; ISS.
 DR GO; GO:0050777; P-negative regulation of immune response; ISS.
 DR GO; GO:0046329; P-negative regulation of JNK cascade; ISS.
 DR GO; GO:0007565; P-pregnancy; ISS.
 DR InterPro; IPR002968; A1-microglobulin.
 DR InterPro; IPR011038; Calycin.
 DR InterPro; IPR002345; Lipocalin.
 DR InterPro; IPR000565; Lipocalin cytochrome P-450.
 DR InterPro; IPR002223; Prot inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00179; BASICPTASE.
 DR PRINTS; PR00179; LIPOCALIN.
 DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 202 Alpha-1-microglobulin.
 FT CHAIN 205 349 Inter-alpha-trypsin inhibitor light chain.
 FT CHAIN 263 343 Trypsatin.
 FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
 FT BINDING 286 336 BPTI/Kunitz inhibitor 2.
 FT BINDING 52 52 Chromophore (By similarity).
 FT BINDING 110 110 Chromophore (By similarity).
 FT BINDING 136 136 Chromophore (By similarity).
 FT BINDING 148 148 Chromophore (By similarity).
 FT DISULFID 90 167 By similarity.
 FT DISULFID 230 280 By similarity.
 FT DISULFID 239 263 By similarity.
 FT DISULFID 255 276 By similarity.
 FT DISULFID 286 336 By similarity.
 FT DISULFID 295 319 By similarity.
 FT DISULFID 311 332 By similarity.
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 233 233 N-linked (GlcNAc...) (potential).
 FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase) (By similarity).
 FT SITE 296 297 Inhibitory (PI) (trypsin) (By similarity).
 FT CONFLICT 142 142 G -> A (in Ref. 2).
 FT CONFLICT 302 302 W -> L (in Ref. 3).
 FT CONFLICT 323 323 G -> N (in Ref. 3).
 FT CONFLICT 330 331 KE -> PK (in Ref. 3).
 FT CONFLICT 334 334 E -> W (in Ref. 3).
 SQ SEQUENCE 349 AA; 38851 MW; 187FB7DCB0824E01 CRC64;

Query Match 78.4%; Score 258; DB 1; Length 349;
 Best Local Similarity 78.2%; Pred. No. 2.1e-22;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 2 ACNLPVIRGPCIAFFPRMADFAYGKCVLPYGGCGGNGNKKFSEKREYCGVP 56
 285 ACNLPVIRGPCIAFFPRMADFAYGKCVLPYGGCGGNGNKKFSEKREYCGVP 339

RESULT 11
 IATR CAPRI STANDARD; PRT; 123 AA.
 AC P62756; P13371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (GIR-14) (Inhibitory fragment of ITI) (Fragment)
 DE ITI (Fragment)
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae; Caprinae; Capra.
 OC Caprine; Capra.
 NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9105540; PubMed=2481505; DOI=10.1016/0167-4838(89)90017-4;
 RA Raap G., Hochstrasser K., Gerl C., Wachter E.;
 RT "Primary structure of a proteinase inhibitor released from goat serum inter-alpha-trypsin inhibitor."
 RT Inter-alpha-trypsin inhibitor."
 RL Biochim. Biophys. Acta 999:335-337(1989).
 CC -I- FUNCTION: This inhibitory fragment, released from native ITI after limited proteolysis with trypsin, contains two homologous domains. Whereas the second domain is a strong inhibitor of trypsin, the first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic elastase.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- MISCELLANEOUS: The amino acid at position p2' (17) appears to determine the specificity of the inhibition of domain I inhibitors with methionine in this position interact weakly with chymotrypsin and elastase; those with leucine interact strongly.
 CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR HSSP; P02760; 1BIK.
 DR InterPro; IPR002223; Prot_inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 DR Direct protein sequencing; Glycoprotein; Plasma; Repeat;
 KW Serine protease inhibitor.
 FT NON_TER 1 1
 FT DOMAIN 5 55 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 61 111 BPTI/Kunitz inhibitor 2.
 FT SITE 15 16 Reactive bond for chymotrypsin and elastase.
 FT SITE 71 72 Reactive bond for trypsin.
 FT DISULFID 5 55 By similarity.
 FT DISULFID 14 38 By similarity.
 FT DISULFID 30 51 By similarity.
 FT DISULFID 61 111 By similarity.
 FT DISULFID 70 94 By similarity.
 FT DISULFID 86 107 By similarity.
 FT CARBOHYD 24 24 N-linked (GlcNAc...).
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13686 MW; 295038173F22D2D1 CRC64;

Query Match 78.1%; Score 257; DB 1; Length 123;
 Best Local Similarity 76.8%; Pred. No. 1.1e-22;
 Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Db 1 EACNLPVIRGPCIAFFPRMADFAYGKCVLPYGGCGGNGNKKFSEKREYCGVP 56
 59 EACNLPVIRGPCIAFFPRMADFAYGKCVLPYGGCGGNGNKKFSEKREYCGVP 114

RESULT 12
 IATR SHEEP STANDARD; PRT; 123 AA.
 AC P62757; P13371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (Inhibitory fragment of ITI) (Fragment).
 DE Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae; Caprinae; Ovis.
 OC Caprine; Ovis.


```

OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=87299012; PubMed=2441725;
RA Raap G., Hochstrasser K., Wachter E., Reisinger P.W.M.;
RT "The amino-acid sequence of the trypsin-released inhibitor from sheep
RL inter-alpha-trypsin inhibitor.";
RL Biochem. Hoppe-Seyler 368:727-731(1987).
CC -1- FUNCTION: This inhibitory fragment, released from native ITI after
CC limited proteolysis with trypsin, contains two homologous domains.
CC Whereas the second domain is a strong inhibitor of trypsin, the
CC first domain interacts weakly with PMN-granulocytic elastase and
CC not at all with pancreatic elastase.
CC -1- MISCELLANEOUS: The amino acid at position p2' (17) appears to
CC determine the specificity of the inhibition of domain I.
CC Inhibitors with methionine in this position interact weakly with
CC chymotrypsin and elastase; those with leucine interact strongly.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC PIR, A29652; A29652.
DR HSSP, P02760; IBIK.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI_2.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Glycoprotein; Plasma; Repeat;
KW Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 5 55 BPTI/Kunitz inhibitor 1.
FT DOMAIN 61 111 BPTI/Kunitz inhibitor 2.
FT SITE 15 16 Reactive bond for chymotrypsin and
FT SITE 71 72 Reactive bond for trypsin.
FT DISULFID 5 55 By similarity.
FT DISULFID 14 38 By similarity.
FT DISULFID 30 51 By similarity.
FT DISULFID 61 111 By similarity.
FT DISULFID 70 94 By similarity.
FT DISULFID 86 107 By similarity.
FT CAROHD 24 24 N-linked (GlcNAc. . .).
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13686 MW; 295038173F2D2D1 CRC64;

Query Match 78.1%; Score 257; DB 1; Length 123;
Best Local Similarity 76.8%; Pred.No.1.le-22;
Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Cy 1 EACNLPYVRGPIAFPPWAFDAVKGKCYLPYGGCGGNGKFKYSEKREYCGVP 56
Db 59 QACNLPYVRGPIAFPPWAFDAVKGKCYLPYGGCGGNGKFKYSEKREYCGIP 114

```

```

RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
RT Mongolian gerbil and Syrian golden hamster in comparison with man and
RT other species.";
RL Biochim. Biophys. Acta 1209:286-292(1994).
RN [2]
RP SEQUENCE OF 205-348, AND SUBUNITS.
RX TISSUE=Plasma, and Urine;
RC MEDLINE=97018241; PubMed=8864857;
RA Yamamoto T., Yamamoto K., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RL hamster urine and plasma.";
RL J. Biochem. 120:145-152(1996).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with Iga
CC and albumin (By similarity).
CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase (By similarity).
CC -1- FUNCTION: Trypsin is a trypsin inhibitor. It inhibits blood
CC coagulation factor Xa and trypsin about 100-fold more rapidly
CC than porcine pancreatic trypsin and chymase. It is a monomer but
CC is also found in mast cells as a complex with cryptase (By
CC similarity).
CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-II) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PTM: The precursor is proteolytically processed into separately
CC functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains a covalently linked brown-
CC yellow chromophore (By similarity).
CC -1- PTM: Heavy chains are interlinked with bikunin via a chondroitin
CC 4-sulfate bridge to the their C-terminal aspartate (By
CC similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, D31814; BA006601.1; -.
DR HSSP, P02760; IBIK.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO; GO:0046904; F:calcium oxalate binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0019862; F:Iga binding; ISS.
DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO; GO:0030236; F:anti-inflammatory response; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0042167; P:heme catabolism; ISS.
DR GO; GO:0050777; P:negative regulation of immune response; ISS.
DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO; GO:0007565; P:pregnancy; ISS.
DR InterPro: IPR002968; A1-microglobln.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin_cytfABP.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.

```

```
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 202 Alpha-1-microglobulin.
FT CHAIN 205 349 Inter-alpha-trypsin inhibitor light
FT chain.
FT CHAIN 262 349 Trypsatin.
FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
FT DOMAIN 286 336 BPTI/Kunitz inhibitor 2.
FT BINDING 52 52 Chromophore (By similarity).
FT BINDING 110 110 Chromophore (By similarity).
FT BINDING 136 136 Chromophore (By similarity).
FT BINDING 148 148 Chromophore (By similarity).
FT BINDING 167 187 By similarity.
FT DISULFID 230 280 By similarity.
FT DISULFID 239 263 By similarity.
FT DISULFID 255 276 By similarity.
FT DISULFID 266 336 By similarity.
FT DISULFID 295 319 By similarity.
FT DISULFID 311 332 By similarity.
FT CARBOHYD 35 35 N-linked (GlcNAc...) (potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (potential).
FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase)
FT SITE 296 297 Inhibitory (PI) (trypsin) (By
FT similarity).
FT CONFLICT 342 342 G -> E (in Ref. 2).
SQ SEQUENCE 349 AA; 38782 MW; 8C954584B7DBE728 CRC64;

Query Match 77.2% Score 254; DB 1; Length 349;
Best Local Similarity 76.4%; Pred. No. 6.2e-22;
Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPVPGPCIAFFPRWAFDAVKGCVLPFYGGCGGNGNKFYSKECKEYCGVP 56
DB 285 ACSLPVPGPCRAVYELWAFDAQGCGVQPSYGGCGGNGNKFYSKECKEYCGVP 339

RESULT 14
ID 070160 PRELIMINARY; PRT; 352 AA.
AC 070160;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-2004 (TrEMBLrel. 26, Last sequence update)
DE Alpha-1-microglobulin/bikunin.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBT_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RA Yoshida K., Suzuki Y., Yamamoto K., Sinohara H.;
RT "Guinea pig alpha1-microglobulin/bikunin: cDNA sequencing, tissue
RT expression and expression during acute phase.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 122:165-172(1999).
CC 1- Similarity: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB006444; BAA25305.1; -.
DR HSSP; P02760; 1BTK.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0018855; F:calcium channel inhibitor activity; ISS.
DR GO; GO:0046904; F:calcium oxalate binding; ISS.
```

```
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0019862; F:IGA binding; ISS.
DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO; GO:0030236; F:anti-inflammatory response; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0042167; P:heme catabolism; ISS.
DR GO; GO:0050779; P:negative regulation of immune response; ISS.
DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO; GO:0007565; P:pregnancy; ISS.
DR InterPro; IPR002968; A1-microglobln.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin cyFPAB.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMCGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN.
SQ SEQUENCE 352 AA; 39033 MW; BAA7447B574C2FAB CRC64;

Query Match 76.9% Score 253; DB 2; Length 352;
Best Local Similarity 78.2%; Pred. No. 8.3e-22;
Matches 43; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 ACNLPVPGPCIAFFPRWAFDAVKGCVLPFYGGCGGNGNKFYSKECKEYCGVP 56
DB 286 ACNLPVPGPCGSAQLWAFDAIKGCVRFYGGCGGNGNKFYSKECKEYCGVP 340

RESULT 15
ID 06P2V8 PRELIMINARY; PRT; 342 AA.
AC 06P2V8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76314.
GN Name=MGC76314;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBT_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Wadon A., Rodriguez S., Sanchez A.,
RA Whiting M., Wadon A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallis D.E., Scherch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
```

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue-embryo:
RA Klein S., Gerard D.S.;
CC Submitted (Dec-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: BC064278; AA64278.1; -.
DR HSSP: P10646; IADZ.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0005810; P:transport; IEA.
DR InterPro: IPR002968; A1-microglobin.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR005566; Lipocalin_cytfabp.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR PRINTS: PR01215; A1MCGLOBULIN.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00179; LIPOCALIN.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00213; LIPOCALIN; 1.
DR Hypothetical protein; Lipocalin.
SQ SEQUENCE 342 AA; 38191 MW; D9B5B825C8B85A CRC64;

Query Match 70.5%; Score 232; DB 2; Length 342;
Best Local Similarity 72.2%; Pred. No. 2.5e-19;
Matches 39; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFPAVDVAVKGCYLFPPYGGCGGNGNKFYSKEKREYCGV 55
Db 280 ACRLEPTGPKCAKTHWAFDAAGKCVTFAYGGCGGNGNQTETEKEKREYCGV 333

RESULT 16
P70004 PRELIMINARY; PRT; 342 AA.
AC P70004:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha1-microglobulin/bikunin precursor (AMBP).
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver:
RA Kawahara A., Hikosaka A., Sasado T., Hirota K.;
RT "Thyroid hormone-dependent repression of alpha1-microglobulin/bikunin
RT (AMBP) gene expression during amphibian metamorphosis.";
RL Dev. Genes Evol. 206:355-362(1997).
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: D87752; BA13453.1; -.
DR HSSP: P02760; IBTK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0005810; P:transport; IEA.
DR InterPro: IPR002968; A1-microglobin.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR005566; Lipocalin_cytfabp.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.

```

```

DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR01215; A1MCGLOBULIN.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00179; LIPOCALIN.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00213; LIPOCALIN; 1.
DR Lipocalin; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 342 Potential.
SQ SEQUENCE 342 AA; 38558 MW; 3050508BDC5C47B CRC64;

Query Match 69.3%; Score 228; DB 2; Length 342;
Best Local Similarity 70.4%; Pred. No. 7.5e-19;
Matches 38; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFPAVDVAVKGCYLFPPYGGCGGNGNKFYSKEKREYCGV 55
Db 280 ACRLEPTGPKCAKTHWAFDAAGKCVTFAYGGCGGNGNQTETEKEKREYCGV 333

RESULT 17
Q7S246 PRELIMINARY; PRT; 342 AA.
ID Q7S246:
AC Q7S246:
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ambp-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Whole;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscil T.B., Toshilyuk S., Carinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney U., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzyzinski M.I., Skalko U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC [2]
RP SEQUENCE FROM N.A.
RC Tissue=Whole;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC Tissue=Whole;
RA Klein S., Strausberg R.;

```

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: BC054142; AA054142.1; -.
DR HSSP: P02760; 1BIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transporter, IEA.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin_cyFABP.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00061; Lipocalin_1.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00213; LIPOCALIN; 1.
KW Lipocalin.
SQ SEQUENCE 342 AA; 38549 MW; BA18FA543B7D4481 CRC64;

Query Match 69.3%; Score 228; DB 2; Length 342;
Best Local Similarity 70.4%; Pred. No. 7.5e-19;
Matches 38; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 ACNLPVHGPGCTAFPPRMAFDVAVKGCYLFPPYGGCGGNGNKFYSKRECYGCV 55
DB 280 ACRLLPTPSPCKTAKTHMAFDAAQGCYLFYSGCGGNGNORYTEKRECYGCV 333

RESULT 18
P78492 PRELIMINARY; PRT; 51 AA.
AC P78492;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inter-alpha-trypsin inhibitor (Fragment).
GN Name=ITIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86025577; PubMed=2413856;
RA Bourguignon J., Diarra-Mehrpour M., Sesboue R., Fraix M.,
RA Sala-Trepat J.M., Martin J.P., Saller J.P.;
RT "Human inter-alpha-trypsin-inhibitor: characterization and partial
nucleotide sequencing of a light chain encoding cDNA.",
RL Biochem Biophys. Res. Commun. 131:1146-1153(1985).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: M11562; AA05194.1; -.
DR HSSP: P02760; 1BIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
FT NON_TER 1
SQ SEQUENCE 51 AA; 5698 MW; C13D74054D45EED2 CRC64;

Query Match 69.0%; Score 227; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 WAFDAVKGKCVLFPPYGGCGGNGNKFYSKRECYGCV 56
DB 2 WAFDAVKGKCVLFPPYGGCGGNGNKFYSKRECYGCV 39

RESULT 19
ID Q7SXH6 PRELIMINARY; PRT; 216 AA.
AC Q7SXH6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Similar to alpha-1-microglobulin/bikunin.
GN ORFNames=sgc.66321;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=whole body;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Biesek S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakestein R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schin J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: BC055598; AA055598.1; -.
DR HSSP: P02760; 1BIK.
DR ZFIN: ZDB-GENE-040426-1608; zgc:66321.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transporter; IEA.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
SQ SEQUENCE 216 AA; 23835 MW; 9E951B4BF0245706 CRC64;

Query Match 62.9%; Score 207; DB 2; Length 216;
Best Local Similarity 64.2%; Pred. No. 1.6e-16;
Matches 34; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 2 ACNLPVHGPGCTAFPPRMAFDVAVKGCYLFPPYGGCGGNGNKFYSKRECYGCV 54
DB 150 ACRLLPMDAGPCAFVDFDLWAFDSSGCKSLTKYGGCGGNGNKFYSKRECYGCV 202

RESULT 20
Q6ZNI4 PRELIMINARY; PRT; 283 AA.
ID Q6ZNI4

```

AC 06ZNI4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Niinomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kaneshiro K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuhara Y., Nagai K., Isogai T.,
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL -i- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AK131196; BAD18391.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin.C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; Ku; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E730986ED30 CRC64;

Query Match 55.3%; Score 182; DB 2; Length 283;
Best Local Similarity 52.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 ACNLPYRGPCIAFPFPMAPDAVKGKCVLPFYGGCGGNGKPFSEKREYGVGP 56
Db 92 ACSLPALQGPCAKVAPFPMAPVNSQTGCQSFYGGCGGNGNPFSEKRECESECPFP 146

RESULT 21
O8TEU8 PRELIMINARY; PRT; 576 AA.
AC O8TEU8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=AFIKXNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=2117322; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Patchy L.;
RA "A human protein containing multiple types of protease-inhibitory
RA modules.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RN SEQUENCE FROM N.A.
RA Trexler M., Banyai L., Patchy L.;
RT "Distinct expression pattern of two related human proteins containing
RT distinct types of protease-inhibitory modules.";
RL Biol. Chem. 383:0-0(2002).
CC -i- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.

```

```

DR EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin.C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; Ku; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4-DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KM Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 55.3%; Score 182; DB 2; Length 576;
Best Local Similarity 52.7%; Pred. No. 3.5e-13;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 ACNLPYRGPCIAFPFPMAPDAVKGKCVLPFYGGCGGNGKPFSEKREYGVGP 56
Db 385 ACSLPALQGPCAKVAPFPMAPVNSQTGCQSFYGGCGGNGNPFSEKRECESECPFP 439

RESULT 22
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Bikunin lig.
GN ORFNames=UNC9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=22887266; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chu C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldeus S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seeshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wiand D., Woods K., Xie M.H., Yanura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -i- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AA088509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.

```

```

DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULFIDE CORE.
DR PRINTS; PR00759; BASICPRASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

```

```

Query Match 55.3%; Score 182; DB 2; Length 576;
Best Local Similarity 52.7%; Pred. No. 3.5e-13;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

```

```

QY 2 ACNLPVIRGPCIAPFPFMAFDVAKGCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 385 ACSLPALQPCAKAYPRMAYNSQTGCGSFYVGCGEGNGNPFESRACESCPCPP 439

```

RESULT 23

```

ID Q7Q0N3 PRELIMINARY; PRT; 571 AA.

```

```

AC Q7Q0N3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-associated serum protein 1.
GN Name=Gaspl.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA MEDLINE=22656519; PubMed=1295574; DOI=10.1210/me.2002-0366;
RA Hill J.C., Qiu Y., Hewick R.M., Wolfman N.M.;
RT "Regulation of myostatin in vivo by growth and differentiation factor-
associated serum protein-1: a novel protein with protease inhibitor
RT and follistatin domains";
RL Mol. Endocrinol. 17:1144-1154(2003).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY308804; AAP72503.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0005175; P:protein binding; IPT.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kunz-m.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.

```

```

DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 571 AA; 63321 MW; B28E676B3DC71256 CRC64;

```

```

Query Match 53.5%; Score 176; DB 2; Length 571;
Best Local Similarity 51.9%; Pred. No. 1.8e-12;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

```

```

QY 3 CNLPVIRGPCIAPFPFMAFDVAKGCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 381 CSLPALQPCAKAYPRMAYNSQTGCGSFYVGCGEGNGNPFESRACESCPCPP 434

```

RESULT 24

```

ID Q7LDW0 PRELIMINARY; PRT; 491 AA.

```

```

AC Q7LDW0;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein RUD2 (Fragment).
GN Name=RUD2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC MEDLINE=21096910; PubMed=1157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tutarelli C., Kearney L., Buckle V.T., Doggett N.A., Flint J.,
RA Higgins D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB006464; AA61237.1; -.
DR HSSP; Q16019; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPRASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR Hypothetical protein.
KW NON_TER
FT NON_TER
SQ SEQUENCE 491 AA; 52710 MW; 0E0954C8DB66206 CRC64;

```

```

Query Match 52.3%; Score 172; DB 2; Length 491;
Best Local Similarity 50.0%; Pred. No. 4.6e-12;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 1 EACNLPVIRGPCIAPFPFMAFDVAKGCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 300 DACULPVGQPCAKAYPRMAYNSQTGCGSFYVGCGEGNGNPFESRACESCPCPP 355

```

RESULT 25


```

Q96NZ8
ID Q96NZ8 PRELIMINARY; PRT; 548 AA.
AC Q96NZ8; Q96NZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative multivalent protease inhibitor WFIKN.
GN Name=WFIKN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyal U., Patchy U.;
RT "A human protein containing multiple types of protease-inhibitory
RT modulee."
RT Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
CC -i- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF422194; AAL18839.1; -.
DR HSSP; P10646; IIRH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; NetCtn.C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP_like.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Protease.
SQ SEQUENCE 548 AA; 58798 MW; 72BB28708D3EFB1F CRC64;

Query Match 52.3%; Score 172; DB 2; Length 548;
Best Local Similarity 50.0%; Pred.No.5.1e-12;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAPPRWAFDAVKGKCVLPYGGGCGGNKPKYSEKREYCGVP 56
DB 357 DACVLPAYVGPGRGWPRWAPSPPLQQCHPFYVGGCGEGNNFHSRSCEDACPVP 412

```

Search completed: February 23, 2005, 03:29:39
Job time : 80 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:35:06 ; Search time 2857 Seconds
(without alignments)
949.770 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIYRGSCIAFFPRWA.....QGNGKFKYSEKREYCVGP 56

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Deiop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPRO_spool/US10038722/runat_18022005_145235_14317/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10038722 @CGN 1.1 4200 @runat_18022005_145235_14317 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEIOP=6 -DELEXT=7

Database : GenEmbl:*

1: gb_da:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	429	6	AX812179 Sequence
2	329	100.0	448	6	163562 Sequence 68
3	324	98.5	8584	6	163561 Sequence 66
4	324	98.5	8590	6	163563 Sequence 70

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	SOURCE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	CDS
1	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
2	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
3	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
4	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"

ALIGNMENTS

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	SOURCE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	CDS
1	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
2	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
3	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"
4	AX812179	Sequence 3 from Patent WO03062431.	AX812179	AX812179.1	GI:38635810	Pichia pastoris	Pichia pastoris	Gerrard, C., Poncin, A., Saudubray, F. and Pechot-Bacque, J.P.		Novel nucleotide sequences, gene constructs, expression vectors and micro-organisms for secreting a protein such as epi-hne-4, and epi-hne-4 protein obtained therefrom	Patent: WO 03062431-A 3 31-JUL-2003;	Location/Qualifiers	1..429 /organism="Pichia pastoris" /mol_type="unassigned DNA" /db_xref="taxon:4922"

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
| | | | |
DB 1212 GCTTCTACTCTCCCATGTCAGAGCTCATGCTCTTCTTCCCAAGATGGGCTTTC 1271
| | | | |
QY 22 AspaIaValIySgIyLysCySvaIleuPheProTyrGlyGlyCySgInGlyAsnGlyAsn 41
| | | | |
DB 1272 GACGCTGTAAAGGGAAGTGGCTTGTCTCCCATGCGGTGTGTCAAGGTAAAGGTAAAC 1331
| | | | |
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
| | | | |
DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 1376
| | | | |
RESULT 5
LOCUS AR022173 198 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5792629.
ACCESSION AR022173
VERSION AR022173.1 GI:3976235
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 198)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Isolated DNA encoding novel protease inhibitory polypeptide
JOURNAL Patent: US 5792629-A 12 11-AUG-1998;
FEATURES
SOURCE Location/Qualifiers
1..198
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 8.37e-29 Length: 198
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 6 Gaps: 0
DB: US-10-038-722-27 (1-56) x AR022173 (1-198)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
| | | | |
DB 10 GCTTCTACTCTCCCATGTCAGAGCTCATGCTCTTCTTCCCAAGATGGGCTTTC 69
| | | | |
QY 22 AspaIaValIySgIyLysCySvaIleuPheProTyrGlyGlyCySgInGlyAsnGlyAsn 41
| | | | |
DB 70 GATGCTGTCAAGGGAAGTGGCTTGTCTCCCATGCGGTGTGTCAAGGTAAAGGTAAAC 129
| | | | |
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
| | | | |
DB 130 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 174
| | | | |
RESULT 6
LOCUS 111653 198 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 12 from Patent US 5409895.
ACCESSION 111653
VERSION 111653.1 GI:909171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 198)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Protease inhibitory polypeptides derived from urinary trypsin
inhibitor and compositions thereof
JOURNAL Patent: US 5409895-A 12 25-APR-1995;
FEATURES
SOURCE Location/Qualifiers
1..198
/organism="unknown"

ORIGIN /mol_type="unassigned DNA"
Alignment Scores: 8.37e-29 Length: 198
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 6 Gaps: 0
DB: US-10-038-722-27 (1-56) x 111653 (1-198)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
| | | | |
DB 10 GCTTCTACTCTCCCATGTCAGAGCTCATGCTCTTCTTCCCAAGATGGGCTTTC 69
| | | | |
QY 22 AspaIaValIySgIyLysCySvaIleuPheProTyrGlyGlyCySgInGlyAsnGlyAsn 41
| | | | |
DB 70 GATGCTGTCAAGGGAAGTGGCTTGTCTCCCATGCGGTGTGTCAAGGTAAAGGTAAAC 129
| | | | |
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
| | | | |
DB 130 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 174
| | | | |
RESULT 7
LOCUS AR268979 204 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 27 from patent US 6500646.
ACCESSION AR268979
VERSION AR268979.1 GI:29699795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 204)
AUTHORS Kuriyama,S. and Hasegawa,T.
TITLE Cell membrane-directed drugs
JOURNAL Patent: US 6500646-A 27 31-DEC-2002;
FEATURES
SOURCE Location/Qualifiers
1..204
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores: 8.61e-29 Length: 204
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 6 Gaps: 0
DB: US-10-038-722-27 (1-56) x AR268979 (1-204)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
| | | | |
DB 4 GCTTCTACTCTCCCATGTCAGAGCTCATGCTCTTCTTCCCAAGATGGGCTTTC 63
| | | | |
QY 22 AspaIaValIySgIyLysCySvaIleuPheProTyrGlyGlyCySgInGlyAsnGlyAsn 41
| | | | |
DB 64 GATGCTGTCAAGGGAAGTGGCTTGTCTCCCATGCGGTGTGTCAAGGTAAAGGTAAAC 123
| | | | |
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
| | | | |
DB 124 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 168
| | | | |
RESULT 8
LOCUS AR022176 209 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 15 from patent US 5792629.
ACCESSION AR022176
VERSION AR022176.1 GI:3976238

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 209)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Isolated DNA encoding novel protease inhibitory polypeptide

JOURNAL Patent: US 5792629-A 15 11-AUG-1998;

FEATURES

source 1..209
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.8e-29 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x AR022176 (1-209)

Qy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21

Db 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCAAGCTCTGGGCATT 69

Qy 22 AppAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnIyAsnGlyAsn 41

Db 70 GATGCTGTCAGAGGAGAGTGCCTCTCCCTACGGGGGCTGCAGGGCAACGGGAAC 129

Qy 42 LysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56

Db 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 9

LOCUS 111656 209 bp DNA linear PAT 26-JUL-1995

DEFINITION Sequence 15 from Patent US 5409895.

ACCESSION 111656

VERSION 111656.1 GI:909174

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 209)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Protease inhibitory polypeptides derived from urinary trypsin

JOURNAL Patent: US 5409895-A 15 25-APR-1995;

FEATURES

source 1..209
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.8e-29 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x 111656 (1-209)

Qy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21

Db 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCAAGCTCTGGGCATT 69

Qy 22 AppAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnIyAsnGlyAsn 41

Db 70 GATGCTGTCAGAGGAGAGTGCCTCTCCCTACCGGGGCTGCCAGGCAACGGGAAC 129

Qy 42 LysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56

Db 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 10

LOCUS AR022172 210 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 11 from patent US 5792629.

ACCESSION AR022172

VERSION AR022172.1 GI:3976234

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 210)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Isolated DNA encoding novel protease inhibitory polypeptide

JOURNAL Patent: US 5792629-A 11 11-AUG-1998;

FEATURES

source 1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x AR022172 (1-210)

Qy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21

Db 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCAAGCTCTGGGCATT 69

Qy 22 AppAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnIyAsnGlyAsn 41

Db 70 GATGCTGTCAGAGGAGAGTGCCTCTCCCTACCGGGGCTGCAGGGCAACGGGAAC 129

Qy 42 LysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56

Db 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 11

LOCUS AR059722 210 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 24 from patent US 5840518.

ACCESSION AR059722

VERSION AR059722.1 GI:5986172

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 210)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE DNA fragment, vector containing the DNA fragment, transformant

JOURNAL Patent: US 5840518-A 24 24-NOV-1998;

FEATURES

source 1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51

Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 99.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x AR059722 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAGAGGGAGAGTGGCTCTTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 12

LOCUS 111652 210 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 11 from Patent US 5409895.
ACCESSION 111652
VERSION 111652.1 GI:909170.
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 210)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Pro tease inhibitor polypeptides derived from urinary trypsin
inhibitor and compositions thereof
JOURNAL Patent: US 5409895-A 11 25-APR-1995;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 99.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x 111652 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAGAGGGAGAGTGGCTCTTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 13

LOCUS 114720 210 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 74 from patent US 5451659.
ACCESSION 114720
VERSION 114720.1 GI:997203
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 210)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Polypeptide, DNA fragment encoding the same, drug composition
containing the same and process for producing the same
JOURNAL Patent: US 5451659-A 74 19-SEP-1995;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 99.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x 114720 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAGAGGGAGAGTGGCTCTTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 14

LOCUS 132807 210 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 74 from patent US 5589360.
ACCESSION 132807
VERSION 132807.1 GI:1823598
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 210)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Polypeptide, DNA fragment encoding the same, drug composition
containing the same and process for producing the same
JOURNAL Patent: US 5589360-A 74 31-DEC-1996;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 99.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x 132807 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAGAGGGAGAGTGGCTCTTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db	130	AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTCGGTGTCCT	174
RESULT 15			
LOCUS	I70519	210 bp	linear
DEFINITION	Sequence 74 from patent US 5679770.		PAT 03-APR-1998
ACCESSION	I70519		
VERSION	I70519.1	GI:3006654	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 210)		
TITLE	Morishita,H., Kanamori,T. and Nobuhara,M.		
JOURNAL	Polypeptide, DNA fragment encoding the same, drug composition		
FEATURES	containing the same and process for producing the same		
source	Patent: US 5679770-A 74 21-Oct-1997;		
	Location/Qualifiers		
	1..210		
ORIGIN	/organism="unknown"		
	/mol_type="unassigned DNA"		
Alignment Scores:			
Pred. No.:	8,84e-29	Length:	210
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0
US-10-038-722-27 (1-56) x I70519 (1-210)			
OY	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe	21
DB	10	GCCTGCACATCTCCCATGATGTCGGGGGCCCTGCGCAGCCTTCATCCAGCTCTGGGCATTT	69
OY	22	AspAlaValIlyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn	41
DB	70	GATGCTGCACAGGGGGAAGTGGCTCTCTTCCCTACGGGGGCTGCGCAGGGCAACCGGAAAC	129
OY	42	LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
DB	130	AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTCGGTGTCCT	174
RESULT 16			
LOCUS	AR022217	295 bp	linear
DEFINITION	Sequence 85 from patent US 5792629.		PAT 05-DEC-1998
ACCESSION	AR022217		
VERSION	AR022217.1	GI:3976279	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 295)		
TITLE	Morishita,H., Kanamori,T. and Nobuhara,M.		
JOURNAL	Isolated DNA encoding novel protease inhibitory polypeptide		
FEATURES	Patent: US 5792629-A 85 11-Aug-1998;		
source	Location/Qualifiers		
	1..295		
ORIGIN	/organism="unknown"		
	/mol_type="unassigned DNA"		
Alignment Scores:			
Pred. No.:	1.21e-28	Length:	295
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x AR022217 (1-295)	
OY	2 AlaGAsanleuPcolleValaArgGlyProCysIleAlaPhePheProArgTmAlaPhe 21
Db	99 GCCGCAATCTCCCAATGATCCCGGGGCCCTGCGCAGCTTCATCCAGCTCTGGGCAATT 158
OY	22 AspaIaValIysGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db	159 GATCTCTGCAAGGGGAAGTGGTCTCTTCCCTCCACGGGGGCTGCCAAGGGGAAC 218
OY	42 LysPheTyrSerGluLysGluCysAspGluTyrCysGlyValPro 56
Db	219 AAGTTCTACTCAGAGAGAGAGTGCAGAGAGTACGCGTGTCTCT 263
RESULT.17	
E04740	E04740 295 bp DNA linear PAT 29-SEP-1997
LOCUS	LOCUS
DEFINITION	DNA encoding novel protease inhibitor.
ACCESSION	E04740
VERSION	E04740.1 GI:2172936
KEYWORDS	JP 1993084083-A/3.
SOURCE	JP 1993084083-A/3.
ORGANISM	synthetic construct
REFERENCE	synthetic construct
AUTHORS	other sequences; artificial sequences.
TITLE	1 (bases 1 to 295)
JOURNAL	Morishita,H., Kanamori,T. and Nobuhara,M.
COMMENT	NEW POLYPEPTIDE, NEW DNA CODING THE SAME POLYPEPTIDE, PRODUCTION OF
	NEW POLYPEPTIDE, NEW MEDICINE COMPOSITION AND NEW ENZYME INHIBITING
	Patent: JP 1993084083-A 3 06-APR-1993;
	MOCHIDA PHARMACEUT CO LTD
	OS Artificial gene
	OC Artificial sequence; Genes.
	OS Escherichia coli
	PN JP 1993084083-A/3
	PD 06-APR-1993
	PF 13-NOV-1991 JP 1991325220
	PR 13-NOV-1990 JP 90P 306745
	PI MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHIRO PC
	C1N1S/15,A61K37/64,A61K37/64,A61K37/64,A61K37/64,A61K37/64, PC
	A61K37/64,
	PC A61K37/64,A61K37/64,A61K37/64,C07K7/10,C12N1/21,C12N9/99, PC
	C12N1S/70,
	PC C12P21/02,(C12N1/21,C12R1:19),(C12P21/02,C12R1:19),C07K9:00;
	CC strandedness: Double;
	CC topology: Linear;
	CC hypothetical: No;
	CC anti-sense: No;
	CC *source: developmental_stage=rearranged;
	CC *source: clone=pw551;
	FH Key
	Location/Qualifiers
	FT 5'UTR 1..26
	FT sig_peptide 27..89
	FT mat_peptide 90..287
	FT
	291..295.
	Location/Qualifiers
	1..295
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
FEATURES	
source	
ORIGIN	
Alignment Scores:	
Pred. No.:	1,21e-28
Score:	296.00
Percent Similarity:	92.73%
Best Local Similarity:	92.73%
Query Match:	89.97%
DB:	6
	Length: 295
	Matches: 51
	Conservative: 0
	Mismatches: 4
	Indels: 0
	Gaps: 0
US-10-038-722-27 (1-56) x E04740 (1-295)	

Qy	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaIlePhePheProArgTrrAlaPhe	21
Db	99	GCTGCATCTCCCATATGCTCGGGGGCCCCCTGCAGCCTTCATCCAGCTCTGGGCATTT	158
Qy	22	AspAlaValIlySGIlyLysCyseValLeuPheProTyrGlyIlyGlyCyseGlnGlyYAsnGlyAsn	41
Db	159	GATGCTGTCCAGAGGAGAGTGCCTCTCTTCCCTTCAGGGGGCTGCACAGGCAACCGGAAC	218
Qy	42	LysPheTyrSerGluIlySGIlyGlyCysArgGlyIlyTyrCyseGlyValPro	56
Db	219	AAGTTCTACTCAGAGAGAGAGTGCAGAGATCTCGGGTGTCCCT	263
RESULT 18	111697		
LOCUS	111697	295 bp	DNA
DEFINITION	Sequence 85 from Patent US 5409895.		linear
ACCESSION	111697		
VERSION	111697.1	GI:909215	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 295)		
AUTHORS	Morishita,H., Kanamori,T. and Nobuhara,M.		
TITLE	Protease inhibitory polypeptides derived from urinary trypsin inhibitor and compositions thereof		
JOURNAL	Patent: US 5409895-A 85 25-APR-1995;		
FEATURES	Location/Qualifiers		
source	1..295		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1,21e-28	Length:	295
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0
US-10-038-722-27 (1-56) x 111697 (1-295)			
Qy	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaIlePhePheProArgTrrAlaPhe	21
Db	99	GCTGCATCTCCCATATGCTCGGGGGCCCCCTGCAGCCTTCATCCAGCTCTGGGCATTT	158
Qy	22	AspAlaValIlySGIlyLysCyseValLeuPheProTyrGlyIlyGlyCyseGlnGlyYAsnGlyAsn	41
Db	159	GATGCTGTCCAGAGGAGAGTGCCTCTCTTCCCTTCAGGGGGCTGCACAGGCAACCGGAAC	218
Qy	42	LysPheTyrSerGluIlySGIlyGlyCysArgGlyIlyTyrCyseGlyValPro	56
Db	219	AAGTTCTACTCAGAGAGAGTGCAGAGATCTCGGGTGTCCCT	263
RESULT 19			
LOCUS	E05909	307 bp	DNA
DEFINITION	E05909		linear
ACCESSION	E05909		
VERSION	E05909.1	GI:2174096	
KEYWORDS	JP 1993308988-A/1.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 307)		
AUTHORS	Morishita,H., Kanamori,T. and Nobuhara,M.		
TITLE	NEW POLYPEPTIDE, NEW DNA, NEW VECTOR, NEW TRANSFORMANT, NEW MEDICINAL COMPOSITION AND PRODUCTION OF THE NEW POLYPEPTIDE		
JOURNAL	Patent: JP 1993308988-A 1 22-NOV-1993;		
COMMENT	MOCHIDA PHARMACEUT CO LTD		
	OS		
	Artificial gene		
	OC		
	Artificial sequence; Genes.		

	OS	Escherichia coli
	PN	JF_1993308988-A/1
	PD	22-NOV-1993
	PF	12-NOV-1992 JP 1992146587
	PI	MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHIRO PC
	C12P21/02_C12N15/00:	
	CC	strandedness: Single;
	CC	topology: linear;
	CC	hypothetical: No;
	CC	anti-sense: No;
	FH	Key Location/Qualifiers
	FT	5'UTR 1..26
	FT	Sig_peptide 27..89
	FT	/product='signal peptide of alkaliphosphatase'
	FT	mat_peptide 90..293
	FT	/product='polypeptide which inhibits protease activity,'
	FT	AN68'
	FT	CDS 27..296
	FT	/product='polypeptide which inhibits protease activity,'
	FT	AN68'
	FT	3'UTR 297..307
	FT	mutation replace(159..'') /product='polypeptide which inhibits protease activity,'
	FT	v26del'
	FT	replace(246..'') /product='polypeptide which inhibits protease activity,'
	FT	v54del'
	FEATURES	
	source	Location/Qualifiers
		1..307
		/organism='synthetic construct'
		/mol_type='genomic DNA'
		/db_xref='taxon:32630'
	ORIGIN	
	Alignment Scores:	
	Pred. No.:	1.26e-28 Length: 307
	Score:	296.00 Matches: 51
	Percent Similarity:	92.73% Conservative: 0
	Best Local Similarity:	92.73% Mismatches: 4
	Query Match:	89.97% Indels: 0
	DB:	Gaps: 0
	US-10-038-722-27 (1-56) x E05909 (1-307)	
Oy	2 AlaCysaenleupProileValarglyProCysillealapheneProargTrpalaphe	21
Dd	93 GCCGTAAATCAACAAATGTCGGGGCCCCCTGCCGAAGCTTCACTCACACTCTGGGCATT	152
Oy	22 AspaIaVallylsgilylvbCyseValleubneProTyrgilygylCyegInglyAasn	41
Dd	153 GATCGTCGACAGGGAGGAGTGCGTCTCTTCCCCTAACGGGGGCGTCCAGAGGCAACGGGAAC	212
Oy	42 lysesheTyrseryglulybglyCvArgglnlyrCyseglyValPro	56
Dd	213 AAGTTCTACTCAGAGAAGAGACTGCAGAGATGCTGGCGGTGTCCT	257
RESULT 20		
LOCUS	AR022209	313 bp DNA linear PAT 05-DEC-1998
DEFINITION	Sequence 75 from patent US 5792629.	
ACCESSION	AR022209	
VERSION	AR022209.1 GI:3976271	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
	1 (bases 1 to 313)	

AUTHORS Morishita, H., Kanamori, T. and Nobuhara, M.
 TITLE Isolated DNA encoding novel protease inhibitory polypeptide
 JOURNAL Patent: US 5792629-A 75 11-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..313
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x AR022209 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCTGGGCATTT 158
 QY 22 AspaIaValIySGIyLVyCysValIeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTyrSerGluIySGIyLVyCysArgGluTyrCysGlyValPro 56
 DB 219 AAGTCTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 263

RESULT 21

LOCUS E04738 313 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding novel protease inhibitor.
 ACCESSION E04738
 VERSION E04738.1 GI:2172934
 KEYWORDS JP 1993084083-A/1.
 SOURCE JP 1993084083-A/1.
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 1 (bases 1 to 313)
 Morishita, H., Kanamori, T. and Nobuhara, M.
 NEW POLYPEPTIDE, NEW DNA CODING THE SAME POLYPEPTIDE, PRODUCTION OF
 NEW POLYPEPTIDE, NEW MEDICINE COMPOSITION AND NEW ENZYME INHIBITING
 Patent: JP 1993084083-A 1 06-APR-1993;
 JOURNAL MOCHIDA PHARMACEUT CO LTD
 COMMENT OS Artificial gene
 OS Artificial sequence; Genes.
 OS Escherichia coli
 PN JP 1993084083-A/1
 PD 06-APR-1993
 PF 13-NOV-1991 JP 1991325220
 PR 13-NOV-1990 JP 90P 306745
 PI MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHITO PC
 C12N15/15, A61K37/64, A61K37/64, A61K37/64, A61K37/64, PC
 A61K37/64,
 PC A61K37/64, A61K37/64, A61K37/64, C07K7/10, C12N1/21, C12N9/99, PC
 C12N15/70,
 PC C12P21/02, (C12N1/21, C12R1:19), (C12P21/02, C12R1:19), C07K99:00;
 CC strandness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: developmental stage=rearranged;
 CC *source: clone=PM552;
 FH Key Location/Qualifiers
 FT 5'UTR 1..26
 FT sig_peptide 27..89
 FT mat_peptide 90..299
 FT /product='novel protease inhibitor' FT 3'UTR
 FT 303..313.

FEATURES

Location/Qualifiers
 source 1..313
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x E04738 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCTGGGCATTT 158
 QY 22 AspaIaValIySGIyLVyCysValIeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTyrSerGluIySGIyLVyCysArgGluTyrCysGlyValPro 56
 DB 219 AAGTCTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 263

RESULT 22

LOCUS 111689 313 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 75 from Patent US 5409895.
 ACCESSION 111689
 VERSION 111689.1 GI:909207
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 unclassified.
 1 (bases 1 to 313)
 Morishita, H., Kanamori, T. and Nobuhara, M.
 Protease inhibitory polypeptides derived from urinary trypsin
 inhibitor and compositions thereof
 Patent: US 5409895-A 75 25-APR-1995;
 JOURNAL Location/Qualifiers
 FEATURES 1..313
 source /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x 111689 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCTGGGCATTT 158
 QY 22 AspaIaValIySGIyLVyCysValIeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTyrSerGluIySGIyLVyCysArgGluTyrCysGlyValPro 56
 DB 219 AAGTCTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 263

RESULT 23

A31027
LOCUS A31027 339 bp DNA linear PAT 21-AUG-1995
DEFINITION DNA for bikunin variant (domain II) from patent EP0401508.
ACCESSION A31027
VERSION A31027.1 GI:1249281
KEYWORDS
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Dae,R.
Proteinaseinhibitors, method for their preparation and
pharmaceutical compositions containing them
Patent: EP 0401508-A 12 12-DEC-1990;
JOURNAL
BAYER AG
FEATURES
source 1..339
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x A31027 (1-339)
QY 2 AAlaCysaenleupProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 10 GCGTGCATCTCCCATAGTCCGGGCGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 69
QY 22 AspaIaValIySgIyLysCySValIleuPheProTyrgIyGlyCySgInGlyAAsnGlyAAsn 41
DB 70 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAC 129
QY 42 LysPheTySerGluLysGluCySArgGluTyrgIyGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTCGGTGTCCT 174
RESULT 24
A31028/c 339 bp DNA linear PAT 21-AUG-1995
LOCUS A31028
DEFINITION DNA for bikunin variant (domain II) from patent EP0401508.
ACCESSION A31028
VERSION A31028.1 GI:1247246
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Dae,R.
Proteinaseinhibitors, method for their preparation and
pharmaceutical compositions containing them
Patent: EP 0401508-A 13 12-DEC-1990;
JOURNAL
BAYER AG
FEATURES
source 1..339
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0

DB: - 6 Gaps: 0
US-10-038-722-27 (1-56) x A31028 (1-339)
QY 2 AAlaCysaenleupProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 330 GCGTGCATCTCCCATAGTCCGGGCGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 271
QY 22 AspaIaValIySgIyLysCySValIleuPheProTyrgIyGlyCySgInGlyAAsnGlyAAsn 41
DB 270 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAC 211
QY 42 LysPheTySerGluLysGluCySArgGluTyrgIyGlyValPro 56
DB 210 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTCGGTGTCCT 166
RESULT 25
BD014127 339 bp DNA linear PAT 27-AUG-2002
LOCUS BD014127
DEFINITION Proteinase inhibitor, process for producing the same, and drug
containing it.
ACCESSION BD014127
VERSION BD014127.1 GI:22554456
KEYWORDS JP 2001112492-A/6.
SOURCE
ORGANISM
synthetic construct
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Dae,R.
Proteinase inhibitor, process for producing the same, and drug
containing it
Patent: JP 2001112492-A 6 24-APR-2001;
JOURNAL
BAYER AG
COMMENT
OS Artificial Sequence
PN JP 2001112492-A/6
PD 24-APR-2001
PF 13-SEP-2000 JP 2000278172
PR 13-MAY-1998 DE P3915689.3 18-JAN-1990 DE P4001244.1 PI
HANS FLITZ, WOLFRANG GEBHARDT, RATHINORA DAS
PC C12N15/09,A61K38/55,A61P1/16,A61P7/00,A61P11/00, PC
A61P13/12,
PC A61P29/00,A61P43/00,C07K14/81,C12N9/99,C12P21/02,C12N15/00, PC
A61K37/64
CC variant of a second domain of bikunin
FH Key
FT source 1..339
Location/Qualifiers
FEATURES
source 1..339
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x BD014127 (1-339)
QY 2 AAlaCysaenleupProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 10 GCGTGCATCTCCCATAGTCCGGGCGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 69
QY 22 AspaIaValIySgIyLysCySValIleuPheProTyrgIyGlyCySgInGlyAAsnGlyAAsn 41
DB 70 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAC 129
QY 42 LysPheTySerGluLysGluCySArgGluTyrgIyGlyValPro 56

Db 130 |||||
AGTCTACTCAGAGAGGAGTGACAGAGTACTGGGTCCT 174

Search completed: February 23, 2005, 05:23:49
Job time : 2867 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 03:14:24 ; Search time 24 Seconds
(without alignments)
174.181 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIVRGSCIAFPFPRWA.....QGNGKFKYSEKREYCVGP 56

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	56	US-08-358-160-20	Sequence 20, Appl
2	329	100.0	141	US-08-358-160-69	Sequence 69, Appl
3	324	98.5	56	US-08-358-160-19	Sequence 19, Appl
4	324	98.5	141	US-08-358-160-69	Sequence 69, Appl
5	296	90.0	57	US-09-144-428-26	Sequence 26, Appl
6	296	90.0	58	US-07-700-526-14	Sequence 11, Appl
7	296	90.0	58	US-08-358-160-3	Sequence 3, Appl
8	296	90.0	58	US-08-358-160-75	Sequence 11, Appl
9	296	90.0	58	US-08-463-155A-39	Sequence 39, Appl
10	296	90.0	58	US-08-463-432B-39	Sequence 39, Appl
11	296	90.0	58	US-08-676-125A-47	Sequence 47, Appl
12	296	90.0	58	US-08-206-310A-39	Sequence 39, Appl
13	296	90.0	58	US-08-398-010A-39	Sequence 39, Appl
14	296	90.0	58	US-08-398-628A-39	Sequence 39, Appl
15	296	90.0	58	US-08-399-115A-39	Sequence 39, Appl
16	296	90.0	58	US-09-136-012A-47	Sequence 47, Appl
17	296	90.0	58	US-08-676-124-78	Sequence 78, Appl
18	296	90.0	58	US-09-414-878-78	Sequence 78, Appl
19	296	90.0	58	US-09-240-136-78	Sequence 78, Appl
20	296	90.0	58	US-09-638-770A-78	Sequence 78, Appl
21	296	90.0	58	PCT-US92-03132-11	Sequence 11, Appl
22	296	90.0	66	US-07-791-213D-8	Sequence 8, Appl
23	296	90.0	66	US-08-293-150A-8	Sequence 8, Appl
24	296	90.0	68	US-07-972-387-76	Sequence 76, Appl
25	296	90.0	68	US-08-431-412-76	Sequence 76, Appl
26	296	90.0	68	US-08-057-971-76	Sequence 76, Appl
27	296	90.0	68	US-08-235-515A-21	Sequence 21, Appl

28	296	90.0	68	US-09-331-793-23	Sequence 23, Appl
29	296	90.0	70	US-07-791-213D-3	Sequence 3, Appl
30	296	90.0	70	US-07-791-213D-6	Sequence 6, Appl
31	296	90.0	70	US-07-972-387-75	Sequence 75, Appl
32	296	90.0	70	US-08-431-412-75	Sequence 75, Appl
33	296	90.0	70	US-08-057-971-75	Sequence 75, Appl
34	296	90.0	70	US-08-293-150A-3	Sequence 3, Appl
35	296	90.0	70	US-08-293-150A-6	Sequence 6, Appl
36	296	90.0	70	US-08-235-515A-25	Sequence 25, Appl
37	296	90.0	87	US-07-791-213D-86	Sequence 86, Appl
38	296	90.0	87	US-08-293-150A-86	Sequence 86, Appl
39	296	90.0	89	US-07-972-387-14	Sequence 14, Appl
40	296	90.0	89	US-08-431-412-14	Sequence 14, Appl
41	296	90.0	89	US-08-057-971-14	Sequence 14, Appl
42	296	90.0	91	US-07-791-213D-76	Sequence 76, Appl
43	296	90.0	91	US-07-791-213D-93	Sequence 93, Appl
44	296	90.0	91	US-07-972-387-4	Sequence 4, Appl
45	296	90.0	91	US-08-431-412-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-358-160-20
; Sequence 20, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: CUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KONITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iyer P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-20

Query Match 100.0%; Score 329; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGCIAFFPRMADFAYKGCYLPFYGGCGGNGKFFYSEKREYCGVP 56
DB 1 EACNLPYRGCIAFFPRMADFAYKGCYLPFYGGCGGNGKFFYSEKREYCGVP 56

RESULT 2
US-08-358-160-69
Sequence 69, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-69

Query Match 100.0%; Score 329; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGCIAFFPRMADFAYKGCYLPFYGGCGGNGKFFYSEKREYCGVP 56
DB 86 EACNLPYRGCIAFFPRMADFAYKGCYLPFYGGCGGNGKFFYSEKREYCGVP 141

RESULT 3
US-08-358-160-19
Sequence 19, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-19

Query Match 98.5%; Score 324; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNPIYVGPCTIAFPFWAFDAVVGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 2 ACNPIYVGPCTIAFPFWAFDAVVGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 4
US-08-358-160-67

Sequence 67, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-67

Query Match 98.5%; Score 324; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNPIYVGPCTIAFPFWAFDAVVGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNPIYVGPCTIAFPFWAFDAVVGKCVLPFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 5
US-09-144-428-26

Sequence 26, Application US/09144428
Patent No. 6583108

GENERAL INFORMATION:
APPLICANT: BAYER CORPORATION, The
APPLICANT: TAMBURINI, Paul P.
APPLICANT: DAVIS, Gary
APPLICANT: DELARIA, Katherine A.
APPLICANT: MARLOR, Christopher W.
APPLICANT: MULLER, Daniel K.
TITLE OF INVENTION: HUMAN BIKUNIN
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,428
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/03894
FILING DATE: 10-MAR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,106
FILING DATE: 11-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,793
FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/725,251
FILING DATE: 04-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: CHAO, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 96,223-11

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-144-428-26

Query Match 90.0%; Score 296; DB 4; Length 57;
Best Local Similarity 92.7%; Pred. No. 8, 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVPGPCIAFPFPAFAVDKVKCVLFPYGGCGGNGNKFSEKREYCGVP 56
DB 3 ACNLPVPGPCRAFIQLWAFDAVKKCVLFPYGGCGGNGNKFSEKREYCGVP 57

RESULT 6
US-07-700-526-11
; Sequence 11, Application US/07700526
; Patent No. 5166133
; GENERAL INFORMATION:
; APPLICANT: Houston, L. L.
; APPLICANT: Kaymakcalan, Zehra
; TITLE OF INVENTION: Method for Inhibiting Adhesion of White
; TITLE OF INVENTION: Blood Cells to Endothelial Cells
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/700,526
; FILING DATE: 19910816
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 2600.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3217
; TELEFAX: (415) 658-5239
; TELEX: 4992659
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-700-526-11

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVPGPCIAFPFPAFAVDKVKCVLFPYGGCGGNGNKFSEKREYCGVP 56
DB 2 ACNLPVPGPCRAFIQLWAFDAVKKCVLFPYGGCGGNGNKFSEKREYCGVP 56

RESULT 7
US-08-358-160-3
; Sequence 3, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-3

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVPGPCIAFPFPAFAVDKVKCVLFPYGGCGGNGNKFSEKREYCGVP 56
DB 4 ACNLPVPGPCRAFIQLWAFDAVKKCVLFPYGGCGGNGNKFSEKREYCGVP 58

RESULT 8
US-08-358-160-75
; Sequence 75, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-75

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23; 4; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPICIAFPFPAWDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 4 ACNLPYVGPICIAFPFPAWDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 58

RESULT 9
US-08-463-155A-39
Sequence 39, Application US/08463155A
Patent No. 5780265
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-463-155A-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23; 4; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPICIAFPFPAWDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 4 ACNLPYVGPICIAFPFPAWDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 58

RESULT 10
US-08-463-432B-39
Sequence 39, Application US/08463432B
Patent No. 5786328
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,432B
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-463-432B-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
|||||
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58
|||||

RESULT 11

US-08-676-125A-47
; Sequence 47, Application US/08676125A
; Patent No. 5795865
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: KALITKEIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive, fifth floor
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word for Windows 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,125A
; FILING DATE: 25 September 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00299
; FILING DATE: 11 January 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,964
; FILING DATE: 11 January 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,264
; FILING DATE: 10 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: DTX-006.2P US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 491-4343
; TELEFAX: (617) 491-8801
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-125A-47

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
|||||
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58
|||||

RESULT 12
US-08-206-310A-39
; Sequence 39, Application US/08206310A
; Patent No. 5795954

; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ DOMAIN
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,310A
; FILING DATE: 04-Mar-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1249
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-206-310A-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
|||||
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58
|||||

RESULT 13
US-08-398-010A-39
; Sequence 39, Application US/08398010A
; Patent No. 5834244

; GENERAL INFORMATION:
; APPLICANT: Robert A. Lazarus and Mark S. Dennis
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
; TITLE OF INVENTION: DOMAIN PROTEINS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,010A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310

FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 32,637
 REFERENCE/DOCKET NUMBER: P0882P1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-398-010A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 56
 Db 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 58

RESULT 14
 US-08-398-628A-39
 Sequence 39, Application US/08398628A
 Patent No. 5863893

GENERAL INFORMATION:
 APPLICANT: Robert A. Lazarus and Mark S. Dennis
 TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
 TITLE OF INVENTION: DOMAIN PROTEINS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/398,628A
 FILING DATE: 03-Mar-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/206310
 FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0882P1-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-398-628A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 56

Db 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 58

RESULT 15
 US-08-399-115A-39
 Sequence 39, Application US/08399115A
 Patent No. 5880256

GENERAL INFORMATION:
 APPLICANT: Robert A. Lazarus and Mark S. Dennis
 TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
 TITLE OF INVENTION: DOMAIN PROTEINS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/399,115A
 FILING DATE: 03-Mar-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/206310
 FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0882P1-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-399-115A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 56
 Db 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGQGNKFKYSEKREYCGVP 58

RESULT 16
 US-09-136-012A-47
 Sequence 47, Application US/09136012A
 Patent No. 5994125
 GENERAL INFORMATION:
 APPLICANT: DYAX CORP
 APPLICANT: MARKLAND, William
 APPLICANT: LADNER, Robert Charles
 TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS
 TITLE OF INVENTION: AND ANALOGUES THEREOF
 NUMBER OF SEQUENCES: 73
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Yankwich & Associates
 STREET: 130 Bishop Allen Drive, fifth floor
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: United States of America

ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,012A
FILING DATE: 17-August-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,125
FILING DATE: 25-September-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00299
FILING DATE: 11-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,264
FILING DATE: 10-March-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,964
FILING DATE: 11-January-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R.
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P.
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-006.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 491-4343
TELEFAX: (617) 491-8801
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-012A-47

Query Match 90.0%; Score 296; DB 2; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYGVGP 56
DB 4 ACNLPVIRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYGVGP 58

RESULT 17
US-08-676-124-78
Sequence 78, Application US/08676124
Patent No. 6010860
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Nelmark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND-3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYGVGP 56
DB 4 ACNLPVIRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYGVGP 58

RESULT 18
US-09-414-878-78
Sequence 78, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265

FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTAFPRNAPDAVKKCVLPFYGGCGGNGNKKFYSEKREYCGVP 56
DB 4 ACNLPYVGPCTAFPRNAPDAVKKCVLPFYGGCGGNGNKKFYSEKREYCGVP 58

RESULT 19
US-09-240-136-78
Sequence 78, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237

NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTAFPRNAPDAVKKCVLPFYGGCGGNGNKKFYSEKREYCGVP 56
DB 4 ACNLPYVGPCTAFPRNAPDAVKKCVLPFYGGCGGNGNKKFYSEKREYCGVP 58

RESULT 20
US-09-638-770A-78
Sequence 78, Application US/09638770A
Patent No. 6423498
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-638-770A-78

Query Match 90.0%; Score 296; DB 4; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56
DB 4 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 58

RESULT 21

PCT-US92-03132-11
Sequence 11, Application PC/TUS9203132
GENERAL INFORMATION:
APPLICANT: Houston, L. L.
APPLICANT: Liu, David Y.
APPLICANT: Kaymakalan, Zehra
TITLE OF INVENTION: Method for Inhibiting Adhesion of White
TITLE OF INVENTION: Blood Cells to Endothelial Cells
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03132
FILING DATE: 19920416
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/700,526
FILING DATE: 14-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 2600.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3217
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03132-11

Query Match 90.0%; Score 296; DB 5; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56
DB 2 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56

RESULT 22

US-07-791-213D-8
Sequence 8, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:

APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuch, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-8

Query Match 90.0%; Score 296; DB 1; Length 66;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56
DB 4 ACNLPVIRGPGCAFPFRAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 58

RESULT 23

US-08-293-150A-8
Sequence 8, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-8

Query Match 90.0%; Score 296; DB 1; Length 66;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPYVGPICIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 4 ACNLPYVGPICIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 58

RESULT 24
US-07-972-387-76
Sequence 76, Application US/07972387
Patent No. 5451659
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5451659uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,387
FILING DATE: 19921105
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345

INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..68
OTHER INFORMATION: //label= sequence
US-07-972-387-76

Query Match 90.0%; Score 296; DB 1; Length 68;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPYVGPICIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 2 ACNLPYVGPICIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 25
US-08-431-412-76
Sequence 76, Application US/08431412
Patent No. 5589360
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5589360uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,412
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,387
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..68
OTHER INFORMATION: //label= sequence

OTHER INFORMATION: /note= "AN68 polypeptide"
US-08-431-412-76

US-08-431-412-76

Query Match	Score	DB 1;	Length
90.0%;	296;	DB 1;	Length 68;
93.7%;	Prod NO	19-22;	

Matches	51;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPVIRGPCIAFFPRWAFDAVKGCVLFPYGGCGGNGNKPFSEKECEHYCGVP 56
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 ACNLPVIRGPCRAFIQLMAFDAYKGCVLFPYGGCGGNGNKPFSEKECREYCGVP 56
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2 ACNLPVIRGPCRAFIQLWAFDAVKGKCVLPYGGCGNGNKKFYSEKECREYCGVP 56

Search completed: February 23, 2005, 03:30:38
Job time : 25 secs

Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 03:28:20 ; Search time 183 Seconds

(without alignments)
357.423 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYIRGPCIAPFPFWA.....QNGNKYSEKREYCGVP 56

Scoring table:

BLOSUM62
Gap0 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA Main:*

```
1: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	329	100.0	56	1 PCT-US03-17665-49	Sequence 49, Appl
2	329	100.0	56	12 US-08-849-406-27	Sequence 27, Appl
3	329	100.0	56	12 US-08-849-406-27	Sequence 27, Appl
4	329	100.0	56	26 US-10-038-722-27	Sequence 27, Appl
5	329	100.0	56	29 US-10-361-997-46	Sequence 40, Appl
6	329	100.0	56	30 US-10-456-986A-49	Sequence 49, Appl
7	329	100.0	56	35 US-10-931-153-23	Sequence 23, Appl
8	329	100.0	141	12 US-08-849-406-74	Sequence 74, Appl
9	329	100.0	141	12 US-08-849-406-74	Sequence 74, Appl
10	329	100.0	141	26 US-10-038-722-27	Sequence 74, Appl
11	329	100.0	655	29 US-10-361-997-59	Sequence 59, Appl
12	329	100.0	655	29 US-10-361-997-51	Sequence 61, Appl
13	329	100.0	694	29 US-10-361-997-71	Sequence 71, Appl
14	329	100.0	728	29 US-10-361-997-75	Sequence 75, Appl
15	329	100.0	729	29 US-10-361-997-46	Sequence 46, Appl
16	329	100.0	752	29 US-10-361-997-74	Sequence 74, Appl
17	329	100.0	753	29 US-10-361-997-45	Sequence 45, Appl
18	324	98.5	56	1 PCT-US03-17665-47	Sequence 47, Appl
19	324	98.5	56	1 PCT-US03-17665-48	Sequence 48, Appl
20	324	98.5	56	12 US-08-849-406-26	Sequence 26, Appl
21	324	98.5	56	12 US-08-849-406-26	Sequence 26, Appl
22	324	98.5	56	26 US-10-038-722-26	Sequence 26, Appl
23	324	98.5	56	30 US-10-456-986A-47	Sequence 47, Appl
24	324	98.5	56	30 US-10-456-986A-48	Sequence 48, Appl
25	324	98.5	58	4 US-08-085-126-5	Sequence 5, Appl
26	324	98.5	58	4 US-08-438-114-5	Sequence 5, Appl
27	324	98.5	141	12 US-08-849-406-72	Sequence 72, Appl
28	324	98.5	141	12 US-08-849-406-76	Sequence 76, Appl
29	324	98.5	141	12 US-08-849-406A-72	Sequence 72, Appl
30	324	98.5	141	12 US-08-849-406A-76	Sequence 76, Appl
31	324	98.5	141	26 US-10-038-722-72	Sequence 72, Appl
32	324	98.5	141	26 US-10-038-722-76	Sequence 76, Appl
33	317	96.4	58	4 US-08-085-126-6	Sequence 6, Appl
34	317	96.4	58	4 US-08-438-114-6	Sequence 6, Appl
35	308	93.6	58	4 US-08-085-126-115	Sequence 115, App
36	308	93.6	58	8 US-08-438-114-115	Sequence 115, App
37	296	90.0	56	35 US-10-931-153-12	Sequence 12, Appl
38	296	90.0	57	16 US-09-218-913D-26	Sequence 26, Appl
39	296	90.0	57	16 US-09-218-913D-26	Sequence 26, Appl
40	296	90.0	57	18 US-09-441-966-26	Sequence 26, Appl
41	296	90.0	57	18 US-09-441-966A-26	Sequence 26, Appl
42	296	90.0	57	18 US-09-441-966B-26	Sequence 26, Appl
43	296	90.0	57	25 US-09-974-026-26	Sequence 26, Appl
44	296	90.0	58	1 PCT-US03-17665-41	Sequence 31, Appl
45	296	90.0	58	3 US-07-687-300-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
PCT-US03-17665-49
Sequence 49, Application PC/TUS0317665
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
APPLICANT: Ladhner, Robert C.
APPLICANT: Lev, Arthur C.
APPLICANT: Hiran, Shliah
APPLICANT: Williams, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001004
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 49
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPI-HNE-4 Sequence
PCT-US03-17665-49

Query Match 100.0%; Score 329; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 2

US-08-849-406-27
Sequence 27, Application US/08849406
APPLICANT: LEY, Arthur C.

LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 56 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-08-849-406-27

Query Match 100.0%; Score 329; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 3
US-08-849-406A-27
Sequence 27, Application US/08849406A
APPLICANT: LEY, Arthur C.

LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 56 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-08-849-406A-27

Query Match 100.0%; Score 329; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56
DB 1 EACNPIYVGRPCIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 4

US-10-038-722-27
Sequence 27, Application US/10038722
GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: LADNER, Robert C.

TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS

FILE REFERENCE: LEY-1B

CURRENT APPLICATION NUMBER: US/10/038,722

CURRENT FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 08/849,406

; PRIOR FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: PCT/US95/16349
 ; PRIOR FILING DATE: 1995-12-15
 ; PRIOR APPLICATION NUMBER: US 08/358,160
 ; PRIOR FILING DATE: 1994-12-16
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Epi-HNE-4
 US-10-038-722-27

Query Match 100.0%; Score 329; DB 26; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 Db 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 5
 US-10-361-997-40
 ; Sequence 40, Application US/10361997
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Ley, Arthur C.
 ; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
 ; FILE REFERENCE: 3421,1015-000
 ; CURRENT APPLICATION NUMBER: US/10/361,997
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,547
 ; PRIOR FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Polypeptide sequence
 US-10-361-997-40

Query Match 100.0%; Score 329; DB 29; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 Db 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 6
 US-10-456-986A-49
 ; Sequence 49, Application US/10456986A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: Hiran, Shitish
 ; APPLICANT: Williams, Anthony
 ; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
 ; FILE REFERENCE: 3421,1001-002
 ; CURRENT APPLICATION NUMBER: US/10/456,986A
 ; CURRENT FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 60/387,239
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: 60/407,003
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: EPI-HNE-4 Sequence
 US-10-456-986A-49

Query Match 100.0%; Score 329; DB 30; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 Db 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 7
 US-10-931-153-23
 ; Sequence 23, Application US/10931153
 ; GENERAL INFORMATION:
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Stochl, Mark
 ; TITLE OF INVENTION: POLY-PREGYLATED PROTEASE INHIBITORS
 ; FILE REFERENCE: 10280-119001
 ; CURRENT APPLICATION NUMBER: US/10/931,153
 ; CURRENT FILING DATE: 2004-08-30
 ; PRIOR APPLICATION NUMBER: US 60/498,845
 ; PRIOR FILING DATE: 2003-08-29
 ; PRIOR APPLICATION NUMBER: US 60/598,967
 ; PRIOR FILING DATE: 2004-08-04
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated peptide
 US-10-931-153-23

Query Match 100.0%; Score 329; DB 35; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 Db 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 8
 US-08-849-406-74
 ; Sequence 74, Application US/08849406
 ; APPLICANT: Ley, Arthur C.
 ; LADNER, Robert C.
 ; GUTERMAN, Sonia K.
 ; ROBERTS, Bruce L.
 ; MARKLAND, William
 ; KENT, Rachel B.
 ; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
 ; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 ; STREET: 624 Ninth Street, N.W. Suite 300
 ; CITY: Washington
 ; STATE: District of Columbia
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/849,406
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-08-849-406-74

Query Match 100.0%; Score 329; DB 12; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.6e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 56
Db 86 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 141

RESULT 9
US-08-849-406A-74
Sequence 74, Application US/08849406A
APPLICANT: LEY, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-08-849-406A-74

Query Match 100.0%; Score 329; DB 12; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.6e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 56
Db 86 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 141

RESULT 10
US-10-038-722-74
Sequence 74, Application US/10038722
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO 74
LENGTH: 141
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BacBI-AatII-EcoRI cassette for expression of Epi-HNE-4 (Table 252
US-10-038-722-74

Query Match 100.0%; Score 329; DB 26; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.6e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 56
Db 86 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGKFFYSEKREYCGVP 141

RESULT 11
US-10-361-997-59
Sequence 59, Application US/10361997
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the N-terminal
; OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion protein
US-10-361-997-59

```

```

Query Match          100.0%; Score 329; DB 29; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56

```

```

RESULT 12
US-10-361-997-61
; Sequence 61, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the C-terminal
; OTHER INFORMATION: albumin-(GGG)4GG-DX-890 fusion protein
US-10-361-997-61

```

```

Query Match          100.0%; Score 329; DB 29; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 600 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 655

```

```

RESULT 13
US-10-361-997-71
; Sequence 71, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoded by NotI cassette of
; OTHER INFORMATION: pDB2300X2 with DX890 (Nterm) and Cterm linker
; OTHER INFORMATION: ready for second DX890

```

US-10-361-997-71

```

Query Match          100.0%; Score 329; DB 29; Length 694;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 25 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 80

```

```

RESULT 14
US-10-361-997-75
; Sequence 75, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of
; OTHER INFORMATION: DX-890::(GGG)4GG::HA::(GGG)4GG::DX890
US-10-361-997-75

```

```

Query Match          100.0%; Score 329; DB 29; Length 728;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56

```

```

RESULT 15
US-10-361-997-46
; Sequence 46, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Secreted product
US-10-361-997-46

```

```

Query Match          100.0%; Score 329; DB 29; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 51; Gaps 0;

```

```

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 674 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 729

```

Thu Feb 24 06:30:13 2005

us-10-038-722-27.rapm

Page 6

Search completed: February 23, 2005, 03:34:59
Job time : 185 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 03:10:59 ; Search time 23 Seconds
(without alignments)
234.267 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYVRGPCIAPFFPRWA.....QGNNGKFKYSEKREYCGVP 56

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296	90.0	352	1	HCHU
2	272	82.7	337	1	TIHGBI
3	269	81.8	352	1	TIHGBI
4	264	80.2	125	1	TIHGBI
5	261	79.3	349	2	S35708
6	258	78.4	349	2	S21089
7	257	78.1	123	2	A29652
8	155	47.1	111	2	S41082
9	155	47.1	751	2	A49974
10	155	47.1	763	2	A49321
11	155	47.1	765	2	S42880
12	154	46.8	252	2	JG0185
13	152	46.2	355	1	S22181
14	151	45.9	62	2	S07451
15	150	45.6	76	2	S04855
16	150	45.6	100	2	A32282
17	148	45.0	64	2	A41399
18	146	44.4	76	2	S06678
19	146	44.4	76	2	S03607
20	146	44.4	484	4	A32761
21	146	44.4	770	1	QRHUA4
22	146	44.4	2225	2	T26063
23	144	43.8	922	2	T23573
24	140	42.6	55	2	S30332
25	138	41.9	61	1	TIWITI
26	138	41.9	747	2	JH0773
27	138	41.9	2167	2	T34395
28	136	41.3	61	1	TIHCBP
29	135	41.0	56	2	JN0380

30	135	41.0	65	1	TIWIVC	venom basic protei
31	134	40.7	1558	2	C89114	short C37C3.6a f
32	133	40.4	57	2	B59399	protein epsilon-dend
33	133	40.4	59	1	TIHGBI	venom basic protei
34	133	40.4	59	2	A59399	long epsilon-dendr
35	133	40.4	122	1	A55115	uterine plasmin/tr
36	133	40.4	3176	2	C8HUA3	collagen alpha 3(V
37	132	40.1	58	1	TIHABK	isoinhibitor K (BP
38	132	40.1	372	2	JC2556	alpha-1-microglobu
39	129	39.2	235	2	A54951	tissue factor path
40	129	39.2	299	2	I46937	tissue factor path
41	129	39.2	300	2	S12143	lipoprotein-associ
42	128	38.9	67	1	TIHBOC	trypsin inhibitor,
43	127	38.6	63	1	TIHFAV	acrosin inhibitor
44	126	38.3	57	1	TIHFAV	venom basic protei
45	126	38.3	62	2	A44180	taicatoxin serine

ALIGNMENTS

RESULT 1

HCHU

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human

N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pr

N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1992 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P0450; B39079; A61580; B25

3217

R:Vertr, H.; Gebhard, W.

A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.

A:Reference number: S13433; MUID:91214554; PMID:1708673

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-352 <VENT>

A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38585.1; PID:G82561

R:Diarrhea-Mehrpour, M.; Bourguignon, J.; Seebouee, R.; Saller, J.P.; Leveillard, T.; Mart

Eur. J. Biochem. 191, 131-139, 1990

A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene

A:Reference number: S10778; MUID:90336621; PMID:1696200

A:Accession: S10778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-202 <DIA>

R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.

Nucleic Acids Res. 14, 7839-7850, 1986

A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-

A:Reference number: A93642; MUID:87040757; PMID:2430261

A:Accession: A93642

A:Molecule type: mRNA

A:Residues: 1-352 <KAU>

A:Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:G24479

Arch. Biochem. Biophys. 228, 544-554, 1984

A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge

A:Reference number: A90074; MUID:84126849; PMID:6198962

A:Accession: A90074

A:Molecule type: protein

A:Residues: 20-56,58-202 <LOP>

A:Experimental source: individual with tubular proteinuria

A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het

R:Tagaki, T.; Takagi, K.; Kawai, T.

Biochem. Biophys. Res. Commun. 98, 997-1001, 1981

A:Title: Complete amino acid sequence of human alpha-1-microglobulin.

A:Reference number: A90225; MUID:81184038; PMID:6164372

A:Accession: A90225

A:Molecule type: protein

A:Residues: 20-47,58-136,138-141,'T',143-144,146-198 <TKA>

A:Experimental source: pooled urine of patients with tubular proteinuria

R.Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Sallier, J.P.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
 A>Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
 A:Reference number: A50686; PMID:8522568; PMID:2408638
 A:Accession: A50686
 A:Molecule type: protein
 A:Residues: 206-290, 'YI', 293-342, 'E', 344-350 <RE1>
 R.Altman, F.; Lacom, B.; Strecker, P.; Parvy, P.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
 A>Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ch
 A:Reference number: PNO450; PMID:93221481; PMID:8466493
 A:Accession: PNO450
 A:Molecule type: protein
 A:Residues: 206-214, 'X' <ATM1>
 R.Englind, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A>Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
 A:Reference number: A59079; PMID:91093267; PMID:1898736
 A:Accession: B39079
 A:Molecule type: protein
 A:Residues: 206-225 <ENG1>
 R.Chiriac, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
 Int. J. Biochem. 23, 1201-1203, 1991
 A>Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhi
 A:Reference number: A61580; PMID:92175157; PMID:1794445
 A:Accession: A61580
 A:Molecule type: protein
 A:Residues: 214, 'X', 216-222, 'X' <CH1>
 R.McKeenan, W.L.; Sakagami, Y.; Hoehn, H.; McKeenan, K.A.
 J. Biol. Chem. 261, 5378-5383, 1986
 A>Title: Two apparent human endocytelial cell growth factors from human hepatoma cells ar
 A:Reference number: A92583; PMID:86168278; PMID:3007499
 A:Accession: B25604
 A:Molecule type: protein
 A:Residues: 206-218, 'X', 216-230, 'X', 232-238, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
 R.Englind, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A>Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
 A:Reference number: A92736; PMID:89380192; PMID:2476436
 A:Accession: C34245
 A:Molecule type: protein
 A:Residues: 206-225 <ENG2>
 R.Tiraboni, C.; Cortese, R.
 Nucleic Acids Res. 14, 6340, 1986
 A>Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobu
 A:Reference number: A25303; PMID:86312901; PMID:2428011
 A:Accession: A25303
 A:Molecule type: mRNA
 A:Residues: 1-218, 'HW' <TRA>
 A>Note: this mRNA sequence appears to contain errors after residue 218
 R.Calero, M.; Escaribano, J.; Grubb, A.; Mendez, E.
 J. Biol. Chem. 269, 384-389, 1994
 A>Title: Location of a novel type of interpolyptide chain linkage in the human protei
 A:Reference number: A53110; PMID:94103241; PMID:7506257
 A:Accession: A53110
 A:Molecule type: protein
 A:Residues: 45-57 <CAL1>
 R.Verr, H.; Kogler, M.; Gebhard, W.
 FEBS Lett. 245, 137-140, 1989
 A>Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inh
 A:Reference number: S03552; PMID:89171290; PMID:2466696
 A:Accession: S03552
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 206-352 <VET2>
 R.Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Pourn
 Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
 A>Title: The heavy chain of human plasma inter-alpha-trypsin inhibitor: their isolation
 A:Reference number: S28928; PMID:93039735; PMID:1384548
 A:Accession: S28930
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-215 <MML>

R.Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fournet
 Eur. J. Biochem. 221, 881-888, 1994
 A>Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
 A:Reference number: S43466; PMID:94229087; PMID:7533643
 A:Accession: S43466
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-221 <MOR>
 R.Miniowski, H.G.; Burgess, M.H.; Oppenheim, J.D.; Vilcek, J.
 Biochemistry 33, 7423-7429, 1994
 A>Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
 A:Reference number: A53642; PMID:94271799; PMID:7516184
 A:Accession: A53642
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-217 <MIS>
 R.Calero, M.; Mendez, E.; Garcia, E.
 Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
 A>Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
 A:Reference number: S55688; PMID:95284116; PMID:7539295
 A:Accession: S55688
 A:Molecule type: protein
 A:Residues: 20-24 <CHL2>
 R.Bourguignon, U.; Diarra-Mehrpour, M.; Sebbou, R.; Frain, M.; Sala-Trepat, J.M.; Marti
 Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
 A>Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide se
 A:Reference number: I52208; PMID:86025577; PMID:2413856
 A:Accession: I52208
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 302-352 <BOU>
 A:Cross-references: GB:M1562; NID:G186587; PIDN:AAA59194.1; PID:G307077
 R.Mojcik, E.G.C.; Van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
 Biochem. J. 311, 753-759, 1995
 A>Title: Factor IX zutphen: a Cys(18) -> Arg mutation results in formation of a heterodi
 A:Reference number: S59509; PMID:96067589; PMID:7487923
 A:Accession: S59509
 A:Molecule type: protein
 A:Residues: 27-35, 'Y', 37 <MOJ>
 R.Altman, F.; Mizon, J.; Khan, S.R.
 Eur. J. Biochem. 236, 984-990, 1996
 A>Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain
 A:Reference number: S66434; PMID:96270753; PMID:8665922
 A:Accession: S66434
 A:Molecule type: protein
 A:Residues: 206-214, 'X', 216-230 <ATM2>
 R.Akerstrom, B.; Bratt, T.; Englund, J.J.
 FEBS Lett. 362, 50-54, 1995
 A>Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cel
 A:Reference number: S68728; PMID:95212582; PMID:7535251
 A:Accession: S68728
 A:Molecule type: protein
 A:Residues: 89-100 <AKE>
 R.Jessen, T.E.; Faarvang, K.L.; Ploug, M.
 FEBS Lett. 230, 195-200, 1988
 A>Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a nc
 A:Reference number: S02431; PMID:88167187; PMID:2450785
 A:Accession: S02431
 A:Molecule type: protein
 A:Residues: 206-214, 'X', 216-217 <JES>
 R.Lopez, C.; Grubb, A.; Mendez, E.
 FEBS Lett. 144, 349-353, 1982
 A>Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequ
 A:Reference number: A91304
 A:Contents: annotation; variant of alpha-1-microglobulin
 A>Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys an
 R.Hochstrasser, K.; Schobberger, O.L.; Rosenblatt, I.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
 A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
 A:Reference number: A51698; PMID:82074265; PMID:6171497
 A:Contents: annotation; carbohydrate binding sites
 R.Moril, M.; Travis, J.

A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01210
A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:Cross-references: UNIPROT:P04365
R:Veeragavan, K.; Singu, K.; Wachter, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; MUID:92328813; PMID:1627153
A:Accession: A45653
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', '14-33 <VEE>
A:Cross-references: PIDN:AB22430.1; PID:9250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBI:P107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
d elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/inhibitory site: leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 80.2%; Score 264; DB 1; Length 135;
Best Local Similarity 78.2%; Pred. No. 9,5e-25;
Matches 43; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 56
DB 62 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 116

RESULT 5
S35708
alpha-1-microglobulin / bikunin precursor - mouse
N:Alternate names: alpha 1-microglobulin / inter-alpha-trypsin inhibitor light chain
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A:Accession: S35708; MUID:93363639; PMID:7689339
R:Chan, P.; Salier, J.P.
Biochim. Biophys. Acta 1174, 195-200, 1993
A:Title: Mouse alpha-1-microglobulin/bikunin precursor: cDNA analysis, gene evolution an
A:Reference number: S35708; MUID:93363639; PMID:7689339
A:Accession: S35708
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <CHA>
A:Cross-references: UNIPROT:O07456; EMBL:X68680; NID:g311702; PIDN:CAA48640.1; PID:g3117
R:Itch, H.; Ide, H.; Kataoka, H.; Tomita, M.; Yoshinara, H.; Nawa, Y.
J. Biochem. 116, 767-772, 1994
A:Title: cDNA sequencing of mouse alpha1-microglobulin/inter-alpha-trypsin inhibitor lig
A:Reference number: JX0355; MUID:95189774; PMID:7533761
A:Accession: JX0355
A:Molecule type: mRNA
A:Residues: 1-64, 'S', '66-349 <ITO>
A:Cross-references: DBJ:D28812; NID:g556530; PIDN:BA05973.1; PID:g556531
A:Experimental source: liver
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: glycoprotein; inflammation; serine proteinase inhibitor
F:34-187/Domain: lipocalin homology <LIP>
F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.3%; Score 261; DB 2; Length 349;
Best Local Similarity 78.2%; Pred. No. 5.6e-24;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 56
DB 285 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 339

RESULT 6
S21089
alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat
N:Alternate names: acid-stable proteinase inhibitor; bikunin; trypstatin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
A:Accession: S21089; A53056; A25935; A31890; A61633
R:Lindqvist, A.; Bratt, T.; Altieri, M.; Kastrup, W.; Akerstrom, B.
Biochim. Biophys. Acta 1130, 63-67, 1992
A:Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of inte
A:Reference number: S21089; MUID:92182014; PMID:1371936
A:Accession: S21089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <LIN>
A:Cross-references: UNIPROT:O64240; GB:S67544; NID:g247162; PIDN:AB21782.1; PID:g247163
R:Itch, H.; Ide, H.; Ishikawa, N.; Nawa, Y.
J. Biol. Chem. 269, 3818-3822, 1994
A:Title: Mast cell proteinase inhibitor, trypstatin, is a fragment of inter-alpha-trypsin
A:Reference number: A53056; MUID:94148892; PMID:7508921
A:Accession: A53056
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 285-341 <ITO>
R:Kaestem, W.; Bjorck, L.; Akerstrom, B.
J. Biol. Chem. 261, 15070-15074, 1986
A:Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in ti
A:Reference number: A25935; MUID:87033744; PMID:2429963
A:Accession: A25935
A:Molecule type: protein
A:Residues: 141, 'A', '143-195 <KAS>
R:Kido, H.; Yokogoshi, Y.; Katunuma, N.
J. Biol. Chem. 263, 18104-18107, 1988
A:Title: Kunitz-type proteinase inhibitor found in rat mast cells. Purification, propertie
A:Reference number: A31890; MUID:89053978; PMID:3263966
A:Accession: A31890
A:Molecule type: protein
A:Residues: 283-301, 'L', '303-322, 'N', '324-329, 'PK', '332-333, 'W', '335-343 <KID>
R:Suzuki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mihara, H.
Inflammation 15, 281-289, 1991
A:Title: Acid-stable proteinase inhibitor in chronic phase of carrageenin-induced inflamma
A:Reference number: A61633; MUID:92120777; PMID:1769732
A:Accession: A61633
A:Molecule type: protein
A:Residues: 205-213, 'X', '215-229, 'N', '231-232, 'K', '234-238 <SUG>
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; sein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-202/Product: alpha-1-microglobulin #status predicted <AIM>
F:34-187/Domain: lipocalin homology <LIP>
F:205-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:24/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:52/Cross-link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to
F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:214/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
F:296/Inhibitory site: Arg (trypsin) #status predicted

Query Match 78.4%; Score 258; DB 2; Length 349;
Best Local Similarity 78.2%; Pred. No. 1.3e-23;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 56
DB 285 ACNLPYVGPICIAFPFPAVDVAVKCVLPFYGGCGGNGNKFYSKRECYGVP 339

```

RESULT 7
A29652
inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29652
R/Raad, G.; Hochstrasser, K.; Machter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
A/Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha
sin inhibitor, XI.1.
A/Reference number: A29652; MUID:87299012; PMID:2441725
A/Accession: A29652
A/Molecule type: protein
A/Residues: 1-123 <RAS>
A/Cross-references: UNIPROT:P13371
C/Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C/Keywords: serine proteinase inhibitor
F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match          78.1%; Score 257; DB 2; Length 123;
Best Local Similarity 76.8%; Pred. No. 6,6e-24;
Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 EACNLPYRGPCIAFFPRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKRECYC 56
Db 59 QACNLPYRGPCRAIGELMAFDVAVKGCYRFYGGCGGNGNPFYQKCKEYCGIP 114

RESULT 8
S41082
amyloid precursor protein homolog - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S41082
R/Petersen, L.C.; Bjorn, S.E.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A/Title: Expression, purification and characterization of a Kunitz-type protease inhibit
A/Reference number: S41082; MUID:94139895; PMID:8307156
A/Accession: S41082
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-111 <PEP>
A/Cross-references: UNIPROT:Q7MAL3
F/59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          47.1%; Score 155; DB 2; Length 111;
Best Local Similarity 54.9%; Pred. No. 1.3e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CNLPYRGPCIAFFPRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKRECYC 53
Db 59 CSQEAHTGPCRAVMPRWYFDLSKGCYRFYGGCGGNNNNFSESDYCNVAVC 109

RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49974
R/Stunt, H.H.; Thirakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A/Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A/Reference number: A49974; MUID:94132029; PMID:8300594
A/Accession: A49974
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-751 <SLD>
A/Cross-references: UNIPROT:Q60709; GB:U15571; NID:G558467; PIDN:AAA50603.1; PID:G558468
A/Note: sequence extracted from NCBI backbone (NCBI:P144636)
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

```

```

F/310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          47.1%; Score 155; DB 2; Length 751;
Best Local Similarity 54.9%; Pred. No. 7.4e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CNLPYRGPCIAFFPRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKRECYC 53
Db 310 CSQEAHTGPCRAVMPRWYFDLSKGCYRFYGGCGGNNNNFSESDYCNVAVC 360

RESULT 10
A49321
amyloid beta (A4) homolog 2 precursor - human
N/Alternate names: CDBI-binding protein
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49321; S34644; S40519
R/Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A/Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A/Reference number: A49321; MUID:93250009; PMID:8485127
A/Accession: A49321
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <SPR>
A/Cross-references: UNIPROT:Q06481; GB:S60099; NID:G300168; PIDN:AAC60589.1; PID:G300169
A/Accession: S34644
A/Molecule type: mRNA
A/Residues: 1-763 <VOM>
A/Cross-references: EMBL:Z22572; NID:G394763; PIDN:CAA80295.1; PID:G394764
R/Masco, W.; Gurnahagavatu, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A/Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A/Reference number: S40519; MUID:94035131; PMID:8220435
A/Accession: S40519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <MAS>
A/Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392
A/Genetics:
A/Gene: GDB:APLP2; APLP2
A/Cross-references: GDB:139159; OMIM:104776
A/Map position: 11q23-11q25
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C/Keywords: alternative splicing; transmembrane protein
F/310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          47.1%; Score 155; DB 2; Length 763;
Best Local Similarity 54.9%; Pred. No. 7.5e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CNLPYRGPCIAFFPRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKRECYC 53
Db 310 CSQEAHTGPCRAVMPRWYFDLSKGCYRFYGGCGGNNNNFSESDYCNVAVC 360

RESULT 11
S42880
amyloid precursor-like protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42880; S47528
R/Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A/Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precurs

```

A:Reference number: S42880
 A:Accession: S42880
 A:Molecule type: mRNA
 A:Residues: 1-765 <SAS>
 A:Cross-references: UNIPROT:P15943; EMBL:X77934
 R:Sandbrik, R.; Masters, C.L.; Beyreuther, K.
 Biochim. Biophys. Acta 1219, 167-170, 1994
 A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein prec
 A:Reference number: S47528; MUID:94368849; PMID:8086458
 A:Accession: S47528
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-765 <SAS>
 A:Cross-references: EMBL:X77934
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C:Keywords: alternative splicing
 F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.1%; Score 155; DB 2; Length 765;
 Best Local Similarity 54.9%; Pred. No. 7.6e-11;
 Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCYLFPYGGCGGNGNKFYSEKREYCG 53
 Db 312 CSEAMTGPCRAVWRMYFDLSKGCVRFYGGCGGNNRNFSEEDYCMAYC 362

RESULT 12

hepatocyte growth factor activator inhibitor type 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 15-Mar-2004
 C:Accession: JG0185
 R:Itch, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.
 Biochem. Biophys. Res. Commun. 255, 740-748, 1999
 A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz-ty
 A:Reference number: JG0185; MUID:99160423; PMID:10049781
 A:Accession: JG0185
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-252 <ITO>
 A:Cross-references: GB:AFO99016
 F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 154; DB 2; Length 252;
 Best Local Similarity 47.2%; Pred. No. 3.6e-11;
 Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Oy 1 EACNLPIVRGPCIAFFPRMAFDVAVKGCYLFPYGGCGGNGNKFYSEKREYCG 53
 Db 131 EYCVKRAVTGFCRAAFPRMYDTEKNSCFYGGCGRGNKNSYLSQEACMQHC 183

RESULT 13

gamma-1-microglobulin precursor - plaice
 C:Species: Pleuronectes platessa (plaice)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S22181
 R:Leaver, M.J.
 submitted to the EMBL Data Library, December 1991
 A:Reference number: S22181
 A:Accession: S22181
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-355 <LEA>
 A:Cross-references: UNIPROT:P36992; EMBL:X63762; NID:964233; PIDN:CAA5294.1; PID:964234
 C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 F:37-189/Domain: lipocalin homology <LIP>
 F:236-286/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:292-342/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.2%; Score 152; DB 1; Length 355;

Best Local Similarity 50.9%; Pred. No. 8.7e-11;
 Matches 27; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCYLFPYGGCGGNGNKFYSEKREYCGV 55
 Db 292 CRLPMAPEPTGQPTIMAFDVTSCMPYKDGICQANANQFSAECQYCGV 344

RESULT 14

proteinase inhibitor 5.II - snake-locks sea anemone
 C:Species: Anemonia sulcata (snake-locks sea anemone)
 C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C:Accession: S07451; B27222
 R:Munderer, G.; Machleidt, W.; Fritz, H.
 Meth. Enzymol. 80, 816-820, 1981
 A:Title: The broad-specificity proteinase inhibitor 5.II from the sea anemone Anemonia s
 A:Reference number: S07451
 A:Accession: S07451
 A:Molecule type: protein
 A:Residues: 1-59 <WUN>
 A:Cross-references: UNIPROT:P10280
 A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
 R:Krebs, H.C.; Habermehl, G.G.
 Naturwissenschaften 74, 395-396, 1987
 A:Title: Isolierung und strukturelle Klärung eines haemolytisch aktiven peptids aus der s
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 45.9%; Score 151; DB 2; Length 62;
 Best Local Similarity 49.1%; Pred. No. 2.3e-11;
 Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Oy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCYLFPYGGCGGNGNKFYSEKREYCGV 55
 Db 5 CELPVTGVCRAFRPRRYTSSSKRCEKFTYGGCGGNNRNFTECKKVCV 57

RESULT 15

Alzheimer's disease amyloid A4 protein - mouse (fragment)
 C:Species: Mus musculus domesticus (western European house mouse)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
 C:Accession: S04855
 R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
 Nucleic Acids Res. 17, 5396, 1989
 A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor o
 A:Reference number: S04855; MUID:89345111; PMID:2569770
 A:Accession: S04855
 A:Molecule type: mRNA
 A:Residues: 1-76 <FUK>
 A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:94965; PIDN:CAA33280.1; PID:993013
 C:Note: the authors translated the codon GAT for residue 74 as Val
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
 F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 45.6%; Score 150; DB 2; Length 76;
 Best Local Similarity 50.0%; Pred. No. 3.7e-11;
 Matches 27; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

Oy 1 EACNLPIVRGPCIAFFPRMAFDVAVKGCYLFPYGGCGGNGNKFYSEKREYCG 54
 Db 1 EVCSGQAGTGCRAFMISRWYDVTEGKCVFPYGGCGGNNRNFTEKVCMAVCG 54

RESULT 16

A32282

A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R.Lemaire, H.G.
Submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360
A:Note: alternative splice form APP(695)
R.La Pauci, G.; Lahiri, D.K.; Salton, S.R.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-protein
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AA13654.1; PID:G516074
R.Johnstone, E.M.; Chaney, W.O.; Moore, R.B.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JON>
A:Cross-references: GB:M29270; NID:G178863; PIDN:AA51768.1; PID:G178865
R.Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHMA-D patients
R.Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:G178613; PIDN:AA59502.1; PID:G178616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A:Molecule type: DNA
A:Residues: 1-530 'OMLMPVPAFMFAKVGK' <YOS2>
A:Cross-references: GB:M34875; NID:G178608; PIDN:AA59501.1; PID:G178615
R.Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Accession: A59020
A:Status: annotation: extram
A:Note: revised physical map for reference I39451
Riley, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:G178618; PIDN:AA51727.1; PID:G178620
A:Note: a mutation with 693-Gln is presented
R.Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:G236720; PIDN:AA19991.1; PID:G236721
R.Kantino, K.; Orr, H.T.; Payami, H.; Wiseman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
ataxias, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:G257377; PIDN:AA23645.1; PID:G257378
A:Experimental source: familial Alzheimer disease family 1B
A:Note: sequence extracted from NCBI backbone (NCBI:P115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:G257379; PIDN:AA23646.1; PID:G257380
A:Experimental source: familial Alzheimer disease family 1B
A:Note: sequence extracted from NCBI backbone (NCBI:P115376)
A:Note: this sequence has a silent mutation
R.Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526
A:Note: alternative splice form APP(695)
R.Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:G178539; PIDN:AA51722.1; PID:G178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R.Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:G178706; PIDN:AA35540.1; PID:G178707
A:Experimental source: brain
R.Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 225, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:G177957; PIDN:AA51564.1; PID:G177958
R.Dyck, T.; Westermann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DVR>
R.Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:86122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G28817
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)

R.Ponte, P.; Gonzalez-DeWitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
 A'Accession number: S00925; MUID:8812639; PMID:2893289
 A'Accession: S00925
 A'Molecule type: mRNA
 A'Residuals: 1-344, 1, 365-770 <PO2>
 A'CROSS-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A'Experimental source: glioblastoma cell line
 A'Note: alternative splice form APP(751)
 R.Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashfor
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A'Accession number: A38949; MUID:8812641; PMID:2893291
 A'Accession: A38949
 A'Molecule type: mRNA
 A'Residuals: 287-367 <KIT>
 A'CROSS-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g287611
 A'Experimental source: glioblastoma cell line
 A'Note: alternative splice form APP(751)
 R.Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashfor
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A>Title: Absence of mutation in the beta-amyloid CDNA's cloned from the brains of three F
 A'Accession number: A30320
 A'Accession: A30320
 A'Status: not compared with conceptual translation
 A'Molecule type: mRNA
 A'Residuals: 284-288, 1, 365-770 <VIT1>
 A'Accession: B30320
 A'Status: not compared with conceptual translation
 A'Molecule type: mRNA
 A'Residuals: 122-288, 1, 365-770 <VIT2>
 A'Accession: C30320
 A'Status: not compared with conceptual translation
 A'Molecule type: mRNA
 A'Residuals: 606-770 <VIT3>
 R.Zahn, S.B.; Salin, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A>Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease by
 A'Accession number: A31087; MUID:88124954; PMID:2893379
 A'Accession: A31087
 A'Molecule type: mRNA
 A'Residuals: 507-770 <2A1>
 A'CROSS-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A'Note: the authors translated the codon GAA for residue 599 as GY, ACC for residue 603
 8 as Val, GGG for residue 609 as Asp, AAT for residue 610 as Gly, and GGT for residue 65
 A'Note: the cited Genbank accession number, J03594, is not in release 101.0
 R.Mastere, C.L.; Multaup, G.; Stimm, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.
 Query Match 44.4%; Score 146; DB 1; Length 770;
 Best Local Similarity 48.1%; Pred. No. 9, 3e-10;
 Matches 26; Conservative 4; Mismatches 24; Indels 0; Gaps 0;
 Oy 1 EACNLPYVRGPCIAPFPMAFDVAVKGCYLPYGGCGGNGNKFYSEKRECYC 54
 Db 289 EVCSQOAEATGCPGRAMISWYFVDTGKCPFFYGGCGGNNRNPTEYCMACVCG 342
 RESULT 22
 T26053
 hypothetical protein W01F3.3 - Caenorhabditis elegans
 C'Species: Caenorhabditis elegans
 C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C'Accession: T26053
 R.Cummings, P.
 Submitted to the EMBL Data Library, March 1997
 A'Accession number: Z20145
 A'Accession: T26053
 A'Status: preliminary; translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Residuals: 1-2225 <WIL>
 A'CROSS-references: UNIPROT:Q45881; EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W0
 A'Experimental source: Clone W01F3
 C'Genetics:

A'Gene: CESP:W01F3.3
 A'Map position: 5
 A'Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
 Query Match 44.4%; Score 146; DB 2; Length 2225;
 Best Local Similarity 47.2%; Pred. No. 2, 5e-09;
 Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
 Oy 1 EACNLPYVRGPCIAPFPMAFDVAVKGCYLPYGGCGGNGNKFYSEKRECYC 53
 Db 1121 EKLQVPEGPKCFADRWYVDDGTCPPRYGGCGGNNRNPTEYCMACVHC 1173
 RESULT 23
 T23573
 hypothetical protein K10D3.4 - Caenorhabditis elegans
 C'Species: Caenorhabditis elegans
 C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C'Accession: T23573
 R.McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A'Accession number: Z19762
 A'Accession: T23573
 A'Status: preliminary; translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Residuals: 1-922 <WIL>
 A'CROSS-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K1
 A'Experimental source: clone K10D3
 C'Genetics:
 A'Gene: CESP:K10D3.4
 A'Map position: 1
 A'Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2
 Query Match 43.8%; Score 144; DB 2; Length 922;
 Best Local Similarity 49.0%; Pred. No. 1, 9e-09;
 Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
 Oy 3 CNLPYVRGPCIAPFPMAFDVAVKGCYLPYGGCGGNGNKFYSEKRECYC 53
 Db 411 CKLPREGNCGTYSNRWFMNKTGCEFFISGCGGNNRNPTEYECODYC 461
 RESULT 24
 S30332
 proteinase inhibitor (Kunitz-type) - sea anemone (Stichodactyla helianthus)
 C'Species: Stichodactyla helianthus, Stichodactis helianthus (Caribbean sea anemone)
 C'Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C'Accession: S30332
 R.Antuch, W.; Berndt, K.D.; Chavez, M.A.; Delfin, J.; Wuehrlich, K.
 Eur. J. Biochem. 212, 675-684, 1993
 A>Title: The NMR solution structure of a Kunitz-type proteinase inhibitor from the sea a
 A'Accession number: S30332; MUID:93215644; PMID:8462542
 A'Accession: S30332
 A'Status: preliminary
 A'Molecule type: protein
 A'Residuals: 1-55 <ANT>
 A'CROSS-references: UNIPROT:P31713
 C'Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 42.6%; Score 140; DB 2; Length 55;
 Best Local Similarity 49.0%; Pred. No. 4, 5e-10;
 Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
 Oy 3 CNLPYVRGPCIAPFPMAFDVAVKGCYLPYGGCGGNGNKFYSEKRECYC 53
 Db 3 CSEPKYGRCKGYPRPFYDSGTGKCTPFYGGCGGNGNPFETLHQCAIC 53
 RESULT 25
 T1VIT1
 venom basic proteinase inhibitor I - western sand viper
 N/Alternate names: venom trypsin inhibitor I

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:11:56 ; Search time 389 Seconds

(without alignments)
852.199 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYVRGCIAPFPRWA.....Ys...QGNNGKPYSEKREYCVGP 56

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2.1/USPTO/US10038722/runatc.18022005.145235.14309/app_query.fasta.1.199
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ing -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=pct -NOR=ext -HARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10038722@cgn.1.1.644@runatc.18022005.145235.14309 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database :

```

N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	190	10	ADP42040 Albumin f
2	329	100.0	190	13	ADR90032 C-termina
3	329	100.0	195	10	ADP42039 Albumin f
4	329	100.0	195	13	ADR90031 N-termina
5	329	100.0	207	10	ADP42055 DX-890 DN

6	329	100.0	207	13	ADR90047
7	329	100.0	429	10	ACF04571
8	329	100.0	444	2	AAT35167
9	329	100.0	445	10	ACF04569
10	329	100.0	1965	10	ADP42043
11	329	100.0	1965	10	ADP42041
12	329	100.0	1965	13	ADR90035
13	329	100.0	1965	13	ADR90033
14	329	100.0	3255	10	ADP42053
15	329	100.0	3255	13	ADR90045
16	329	100.0	3440	13	ADR90048
17	329	100.0	3441	10	ADP42056
18	329	100.0	3444	10	ADP42068
19	329	100.0	3444	13	ADR90019
20	324	98.5	8584	2	AAT35166
21	324	98.5	8590	2	AAT35168
22	296	90.0	204	2	AAT79078
23	296	90.0	204	2	AAV40045
24	296	90.0	210	2	AAQ78607
25	296	90.0	210	2	AAQ64758
26	296	90.0	210	2	AAQ64756
27	296	90.0	295	2	AAQ24151
28	296	90.0	307	2	AAQ41875
29	296	90.0	313	2	AAQ24143
30	296	90.0	313	2	AAQ41870
31	296	90.0	339	2	AAQ06879
32	296	90.0	344	2	AAQ54328
33	296	90.0	372	2	AAT79080
34	296	90.0	372	2	AAT79081
35	296	90.0	380	2	AAQ78612
36	296	90.0	408	9	ACH21498
37	296	90.0	435	2	AAT79083
38	296	90.0	441	2	AAV40046
39	296	90.0	467	2	AAT79086
40	296	90.0	467	2	AAT79088
41	296	90.0	530	2	AAT79087
42	296	90.0	645	2	AAT75154
43	296	90.0	666	2	AAT75155
44	296	90.0	1123	6	ABK55655
45	296	90.0	1232	1	AAH81432

ALIGNMENTS

RESULT.1	ADP42040	standard; cDNA, 190 BP.
ID	ADP42040	
XX	ADP42040;	
AC	ADP42040;	
XX		
DT	12-FEB-2004	(first entry)
XX		
DE	Albumin fusion protein-related C-terminal BamHI-HindIII DX-890 cDNA.	
XX		
KW	albumin fusion; Kunitz domain; cytosolic; haemostatic;	
KW	hereditary angioedema; cancer; bleeding; gene therapy; DX-890; ss.	
XX	Unidentified.	
OS		
XX		
PN	WO2003066824-A2.	
XX		
PD	14-AUG-2003.	
XX		
PF	07-FEB-2003; 2003WO-US003616.	
XX		
PR	07-FEB-2002; 2002US-0355547P.	
XX		
PA	(AVET) AVENTIS BEHRING GMBH.	
PA	(AVET) AVENTIS BEHRING LLC.	
PA	(DELZ) DELTA BIOTECHNOLOGY LTD.	
PA	(DYAX-) DYAX CORP.	
XX		
PI	Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;	

PI Ley AC;
XX
XX MPI; 2003-731497/69.
DR
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX
XX Example 23; Page 73; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related C-terminal BamHI-
CC HindIII DX-890 cDNA of the invention.
XX
SQ Sequence 190 BP; 46 A; 30 C; 51 G; 63 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 1,1e-36 Length: 190
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42040 (1-190)
QY 1 GIUALACYSANLEUPROILEVALARGGLYPROCYSIIIEALAPHEPHEPROARGTRPALA 20
DB 13 GAAGCTGTAACCTGCCAATGTTAGAGGTCACATGATGCTTCTTCCCAAGATGGGCT 72
QY 21 PHEAPALAVALLYSGLYVSCYSVALLEUPHEPROTYRGIVGLYCYSGINGLYASNGLY 40
DB 73 TTCGATGCTGTTAAGGTAAGTGTTGTTTCCCATATGGGTGTGTCAAGGTAAAGGT 132
QY 41 AENLYSPHEITYRSEGLULYSGIUCYSARGSLUTYRCYSGIYVALPRO 56
DB 133 AACCAAGTCTACTCTGAAAAAGAAATGTAAGAATACTGTGGTTCCTCA 180
XX
RESULT 2
ADR90032
ID ADR90032 standard; cDNA, 190 BP.
XX
XX ADR90032;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX C-terminal BamHI-HindIII DX-890 cDNA.
DE
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic; DX-890; ss.
XX
XX Unidentified.
OS
XX
XX US2004171794-A1.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 07-FEB-2003; 2003US-00361997.
PF
XX
XX 07-FEB-2003; 2003US-00361997.
PR
XX
XX (LADN/) LADNER R. C.
PA (LEYA/) LEY A C.
PI Ladhner RC, Ley AC;

XX
XX MPI; 2004-625120/60.
DR
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
PT
XX
XX
XX Example 7; SEQ ID NO 57; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytostatic and haemostatic agent. The present sequence is a C-terminal
CC BamHI-HindIII DX-890 cDNA. This sequence is used in the exemplification
CC of the invention.
XX
SQ Sequence 190 BP; 46 A; 30 C; 51 G; 63 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 1,1e-36 Length: 190
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADR90032 (1-190)
QY 1 GIUALACYSANLEUPROILEVALARGGLYPROCYSIIIEALAPHEPHEPROARGTRPALA 20
DB 13 GAAGCTGTAACCTGCCAATGTTAGAGGTCACATGATGCTTCTTCCCAAGATGGGCT 72
QY 21 PHEAPALAVALLYSGLYVSCYSVALLEUPHEPROTYRGIVGLYCYSGINGLYASNGLY 40
DB 73 TTCGATGCTGTTAAGGTAAGTGTTGTTTCCCATATGGGTGTGTCAAGGTAAAGGT 132
QY 41 AENLYSPHEITYRSEGLULYSGIUCYSARGSLUTYRCYSGIYVALPRO 56
DB 133 AACCAAGTCTACTCTGAAAAAGAAATGTAAGAATACTGTGGTTCCTCA 180
XX
RESULT 3
ADF42039
ID ADF42039 standard; cDNA, 195 BP.
XX
XX ADF42039;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Albumin fusion protein-related N-terminal BglII-BamHI DX-890 cDNA.
DE
XX
XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy; DX-890; ss.
KW
XX
XX Unidentified.
OS
XX
XX WO2003066824-A2.
PN
XX
XX 14-AUG-2003.
PD
XX
XX 07-FEB-2003; 2003WO-US003616.
PF
XX
XX 07-FEB-2002; 2002US-0355547P.
PR
XX
XX (AVENT) AVENTIS BEHRING GMBH.
PA (AVENT) AVENTIS BEHRING LLC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (DVAX-) DVAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladhner RC,
PI Ley AC;

DR WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX Example 23; Page 73; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related N-terminal BgIII-
CC BamHI DX-890 CDNA of the invention.

XX Sequence 195 BP; 49 A; 30 C; 53 G; 63 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,14e-36	Length:	195
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-038-722-27 (1-56) x ADF42039 (1-195)

QY 1 GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAACTTCCCAATTGTTAGAGTCCATGATGCTTTTCCCAAGATGGCT 78

QY 21 PheAspAlaValLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 79 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGCTGTGTCAGAGTAAAGCT 138

QY 41 AsnLysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
DB 139 AACCAAGTCTACTCTGAAGAAAGATGTAGAGATCTGTTGTTCCA 186

RESULT 4

ADP90031

ID ADR90031 standard; cDNA; 195 BP.

XX ADR90031;

XX 18-NOV-2004 (first entry)

XX N-terminal BgIII-BamHI DX-890 CDNA.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytosolic; haemostatic; DX-890; ss.

XX Undifferentiated.

XX US2004171794-A1.

XX 02-SEP-2004.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
XX Lader RC, Ley AC;
PI
XX WPI; 2004-625120/60.

XX New Kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX Example 7; SEQ ID NO 56; 123pp; English.

XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPT-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytosolic and haemostatic agent. The present sequence is a N-terminal
CC BgIII-BamHI DX-890 CDNA. This sequence is used in the exemplification of
CC the invention.

XX Sequence 195 BP; 49 A; 30 C; 53 G; 63 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,14e-36	Length:	195
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90031 (1-195)

QY 1 GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAACTTCCCAATTGTTAGAGTCCATGATGCTTTTCCCAAGATGGCT 78

QY 21 PheAspAlaValLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 79 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGCTGTGTCAGAGTAAAGCT 138

QY 41 AsnLysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
DB 139 AACCAAGTCTACTCTGAAGAAAGATGTAGAGATCTGTTGTTCCA 186

RESULT 5

ADP42055

ID ADF42055 standard; DNA; 207 BP.

XX ADF42055;

XX 12-FEB-2004 (first entry)

XX DX-890 DNA which was inserted at BspEI/XbaI site of pDB2300X2.

XX albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy;
KW plasmid pDB2300X2 NotI expression cassette; ds; DX-890.

XX Undifferentiated.

XX WO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING L.L.C.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Lader RC;
PI Ley AC;
XX WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 PT useful for preparing a composition for treating a patient with hereditary
 PT angiodema or angiodema-related disease, cancer or bleeding disorder.
 XX
 PS Example 23; Page 89; 110pp; English.
 CC The invention relates to a novel albumin fusion protein comprising a
 CC Kunitz domain peptide or its fragment or variant and an albumin or its
 CC fragment or variant. The fusion protein of the invention demonstrates
 CC cytotatic and haemostatic activities and may be useful for preparing a
 CC composition for treating a patient with hereditary angiodema, an
 CC angiodema-related disease, cancer, a cancer-related disease or a
 CC bleeding disorder, as well as during gene therapy procedures. The current
 CC sequence is that of the DX-890 DNA of the invention which was inserted at
 CC BspRI/KpnI site of plasmid pDB2300X2 modified NotI expression cassette.
 XX
 SQ Sequence 207 BP; 37 A; 51 C; 59 G; 60 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,23e-36 Length: 207
 Score: 329.00 Matches: 56
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-038-722-27 (1-56) x ADR42055 (1-207)
 QY 1 GIUUAAGYASNLEUPROILEVALARGLYPCQYSLIAPHEPHEPROARGTRPALA 20
 DB 28 GAGGCTTGCAATCTTCCTATCGTCGCGCCCTTGCAATGCGCTTTTCTCGTTGGGCC 87
 QY 21 PHEAPALAVALLVSGLYLVCYSEVALLEUPHEPROTYRGLYGLYCYSEGLNGLYASNGLY 40
 DB 88 TTGACGCGCGCAAGCAAGAAATGCGCTTTTCTTACGGCGGTTGCCAGGCGCAATGCG 147
 QY 41 AENLYSPHEITYRSEKGLULYSGLYCYSEARGGLUTRYCYSEGLVYALPRO 56
 DB 148 AATAAATTTTATAGCGAGAAAGAGTCCCGTAGTATGCGGCGCTCCT 195
 RESULT 6
 ADR90047
 ID ADR90047 standard; cDNA; 207 BP.
 XX
 AC ADR90047;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE DX-890 coding region cDNA.
 XX
 KM Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 KM hereditary angiodema; cancer; chronic obstructive pulmonary disease;
 KM asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KM cytotatic; haemostatic; DX-890; ss.
 XX
 OS Unidentified.
 XX
 PN US2004171794-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 07-FEB-2003; 2003US-00361997.
 XX
 PR 07-FEB-2003; 2003US-00361997.
 XX
 PA (LADN/) LADNER R C.
 PA (LEVA/) LEV A C.
 XX
 PI Ladner RC, Lev AC;
 XX
 DR WPI; 2004-625120/60.
 XX

PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX
 PS Example 19; SEQ ID NO 72; 123pp; English.
 CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated Dpi-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angiodema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytotatic and haemostatic agent. The present sequence is a DX-890 coding
 CC region cDNA. This sequence is used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 207 BP; 37 A; 51 C; 59 G; 60 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,23e-36 Length: 207
 Score: 329.00 Matches: 56
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-10-038-722-27 (1-56) x ADR90047 (1-207)
 QY 1 GIUUAAGYASNLEUPROILEVALARGLYPCQYSLIAPHEPHEPROARGTRPALA 20
 DB 28 GAGGCTTGCAATCTTCCTATCGTCGCGCCCTTGCAATGCGCTTTTCTCGTTGGGCC 87
 QY 21 PHEAPALAVALLVSGLYLVCYSEVALLEUPHEPROTYRGLYGLYCYSEGLNGLYASNGLY 40
 DB 88 TTGACGCGCGCAAGCAAGAAATGCGCTTTTCTTACGGCGGTTGCCAGGCGCAATGCG 147
 QY 41 AENLYSPHEITYRSEKGLULYSGLYCYSEARGGLUTRYCYSEGLVYALPRO 56
 DB 148 AATAAATTTTATAGCGAGAAAGAGTCCCGTAGTATGCGGCGCTCCT 195
 RESULT 7
 ACP04571
 ID ACP04571 standard; DNA; 429 BP.
 XX
 AC ACP04571;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Fusion sequence of alpha mating factor and EPI-hNE-4 coding sequences.
 XX
 KM EPI-hNE-4; EPI-hNE; alpha mating factor prepropeptide; fusion gene; gene;
 KM mutagenic; ds.
 XX
 KM Saccharomyces cerevisiae.
 OS Pichia pastoris.
 XX
 PN WO2003062431-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 23-JAN-2003; 2003WO-EP001212.
 XX
 PR 23-JAN-2002; 2002EP-00290166.
 XX
 PA (DEBI-) DEBIOPHAM SA.
 XX
 PI Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;
 XX
 DR WPI; 2003-598755/56.
 DR P-PsDB; ABR84585.
 XX
 PT New fused gene constructs and expression vectors, useful for transforming
 PT microorganisms (particularly the yeast Pichia pastoris) for use in
 PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly

PF processed form.
XX
XX
PS Claim 3; Fig 9; 27pp; English.
XX
XX The present invention relates to a fused gene construct, which comprises
CC a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n+9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a fusion sequence
CC containing the *S. cerevisiae* alpha mating factor prepeptide coding
CC sequence and the *Pichia pastoris* EPI-hNE-4 coding sequence and used in
CC the exemplification of the invention
XX
SQ Sequence 429 BP; 91 A; 100 C; 102 G; 136 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,196-36 Length: 429
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x ACF04571 (1-429)
QY 1 GluAlaCySaenLeuProIleValArgGlyProCySileAlaPhePheProArgTrrAla 20
Db 256 GAGGCTGTAACTTCCCAATCGTCAGAGTCATCATGCTTCTTCCCAAGATGGGCT 315
QY 21 PheAspAlaValIySGlyLysCyValLeuPheProTyrGlyGlyCySGInGlyAsnGly 40
Db 316 TTCGACGCTTTAAAGGTAAGTGCCTGTTCCATACGGGTGTGTCAGAGTAACGCT 375
QY 41 AsnLysPheTyrSerGluLysGluCySaArgGluTyrCySGIValPro 56
Db 376 AACCAAGTTCTACTCTGAGAAAGAGTGTAGAGAGTACTGTGTTCCTCA 423
RESULT 8
AAT35167
ID AAT35167 standard; DNA; 444 BP.
XX
XX AAT35167;
XX
DT 14-FEB-1997 (first entry)
XX
XX EPI-hNE-4 Modified Kunitz domain expression cassette.
XX
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
XX alpha antitrypsin; respiratory disorder; cystic fibrosis;
XX smokers emphysema; ss.
XX
XX Synthetic.
XX
XX
FH Key Location/Qualifiers
FT CDS 10..435
FT /tag= a
FT /product= "EPI-hNE-4 modified Kunitz domain"
XX
XX MO9620278-A2.
XX
XX 04-JUL-1996.

PF 15-DEC-1995; 95WO-US016349.
XX
XX
PR 16-DEC-1994; 94US-00358160.
XX
XX
PA (PROT-) PROTEIN ENG CORP.
XX
XX
PI Ley AC, Lather RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX
XX WPI, 1996-321851/32.
XX
XX P-PEDB; AAR99215.
XX
XX
PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX
PS Example 10; Page 75; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
XX of pathogens and the restructuring of connective tissue. In cases of
XX reduction of the circulating alpha-1-protease inhibitor (API or alpha
XX antitrypsin), or the inactivation of API by oxidation (smokers
XX emphysema), extensive destruction of the lung tissue may result from
XX uncontrolled elastolytic activity of human neutrophil elastase. Other
XX respiratory disorders such as cystic fibrosis are thought to be caused by
XX human neutrophil elastase release by neutrophils. The genetically
XX engineered human derived Kunitz domains can be used to treat such
XX respiratory disorders. See AAR99146-R99211. Fusion genes were used in the
XX production of the Kunitz domain derivatives. Protein expression cassettes
XX are then cloned into the plasmid pHI-D2 using BstBI and EcoRI
XX restriction sites. The cloned sequence is under the transcriptional
XX control of *Pichia pastoris* axol gene promoter and regulatory sequences
XX and downstream polyadenylation and transcription termination sequences.
XX Transformed strains of *P. pastoris* were used to express the various EPI-
XX hNE proteins derived from the BPT1 and ITI-D2 Kunitz domains. This
XX sequence is a BstBI-AccII-EcoRI expression cassette for expression of EPI-
XX hNE-4
SQ Sequence 444 BP; 98 A; 102 C; 105 G; 139 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,346-36 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x AAT35167 (1-444)
QY 1 GluAlaCySaenLeuProIleValArgGlyProCySileAlaPhePheProArgTrrAla 20
Db 265 GAGGCTGTAACTTCCCAATCGTCAGAGTCATCATGCTTCTTCCCAAGATGGGCT 324
QY 21 PheAspAlaValIySGlyLysCyValLeuPheProTyrGlyGlyCySGInGlyAsnGly 40
Db 325 TTCGACGCTTTAAAGGTAAGTGCCTGTTCCATACGGGTGTGTCAGAGTAACGCT 384
QY 41 AsnLysPheTyrSerGluLysGluCySaArgGluTyrCySGIValPro 56
Db 385 AACCAAGTTCTACTCTGAGAAAGAGTGTAGAGAGTACTGTGTTCCTCA 432
RESULT 9
ACF04569
ID ACF04569 standard; DNA; 445 BP.
XX
XX ACF04569;
XX
XX
DT 04-DEC-2003 (first entry)
XX
XX P. pastoris prepro-EPI-hNE-4 mutated coding sequence.
XX
XX EPI-hNE-4; EPI-hNE; alpha mating factor prepeptide; gene; mutant;
XX

KW mutagenic; ds.
 XX Pichia pastoris.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 10.435
 FT /*tag= a
 FT /product= "mutated prepro-Epi-hNE-4"
 XX
 XX WO2003062431-A2.
 XX 31-JUL-2003.
 XX 23-JAN-2003; 2003WO-EP001212.
 XX 23-JAN-2002; 2002EP-00290166.
 XX (DEBI-) DEBIOPHARM SA.
 XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;
 XX WPI: 2003-598755/56.
 XX P-PSDB; ABR84583.
 XX
 XX New fused gene constructs and expression vectors, useful for transforming
 XX microorganisms (particularly the yeast *Pichia pastoris*) for use in
 XX producing e.g. Epi-hNE-4 proteins with very low levels of its improperly
 XX processed form.
 XX
 XX Example 2; Fig 1B; 27pp; English.
 XX
 XX The present invention relates to a fused gene construct, which comprises
 XX a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
 XX mating factor prepropeptide or its variant, which is modified so as to
 XX replace the lysine residue in position 76 of the amino acid sequence of
 XX the naturally occurring prepropeptide by an Alanine residue. The
 XX nucleotide sequence is ligated to the 5' terminal of a nucleotide
 XX sequence coding for Epi-hNE-4. An expression vector for the sequence is
 XX also claimed. The gene construct or vector is useful for transforming
 XX microorganisms (particularly yeast) to produce Epi-hNE-4 protein with
 XX very low levels of its improperly processed form. The gene construct,
 XX nucleotide sequence, expression vector or microorganism is useful for
 XX producing or secreting a protein, particularly Epi-hNE-4, which contains
 XX undetectable levels of the Epi-hNE-4 (n+9). This facilitates further
 XX purification steps and therefore results in economies both on the
 XX financial and time-spent scale. The present sequence is a mutated version
 XX of the *Pichia pastoris* Epi-hNE-4 coding sequence used in the
 XX exemplification of the invention
 XX
 XX SQ Sequence 445 BP; 96 A; 104 C; 105 G; 140 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 3,34e-36 Length: 445
 XX Score: 329.00 Matches: 56
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 10 Gaps: 0
 XX
 XX US-10-038-722-27 (1-56) x ACF04569 (1-445)
 QY 1 GIUUAACyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTPAla 20
 Db 265 GAGGCTTGAATCTTCCCAATCGTCAGAGGTCATGCAATGCTTCTTCCCAAGATGGGCT 324
 QY 21 PheAspAlaValIleGlyIleCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
 Db 325 TTGACGCTGTAAAGGTAAAGTCGCTTCTTCCCATAGCGGTGTCAAGGTAAAGCT 384
 QY 41 AsnIlePheTyrSerGlyIleCysValLeuArgGlyTyrCysGlyValPro 56
 Db 385 AACCACTTACTCTGAGGAAGGTGTAGAGTACTGTGCTTCCA 432

RESULT 10
 ADF42043
 ID ADF42043 standard; DNA; 1965 BP.
 XX
 XX ADF42043;
 AC 12-FEB-2004 (first entry)
 DT
 XX
 XX C-terminal albumin-(GGS)4GG-DX-890 fusion DNA.
 XX
 XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy;
 KW C-terminal albumin-(GGS)4GG-DX-890 fusion; ds; gene.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH 1.1965
 FT /*tag= a
 FT /partial
 FT /product= "C-terminal albumin-(GGS)4GG-DX-890 fusion
 FT protein"
 FT /note= "No start or stop codon"
 XX
 XX WO2003066824-A2.
 XX 14-AUG-2003.
 XX 07-FEB-2003; 2003WO-US003616.
 XX 07-FEB-2002; 2002US-035547P.
 XX (AVET) AVENTIS BEHRING GMBH.
 XX (AVET) AVENTIS BEHRING LLC.
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX (DYAX-) DYAX CORP.
 XX
 XX Hauser H, Welmer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 PI ley AC;
 XX WPI: 2003-731497/69.
 XX P-PSDB; ADF42044.
 XX
 XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 XX useful for preparing a composition for treating a patient with hereditary
 XX angioedema or angioedema-related disease, cancer or bleeding disorder.
 XX
 XX Example 23; Page 77-76; 110pp; English.
 XX
 XX The invention relates to a novel albumin fusion protein comprising a
 XX Kunitz domain peptide or its fragment or variant and an albumin or its
 XX fragment or variant. The fusion protein of the invention demonstrates
 XX cytostatic and haemostatic activities and may be useful for preparing a
 XX composition for treating a patient with hereditary angioedema, an
 XX angioedema-related disease, cancer, a cancer-related disease or a
 XX bleeding disorder, as well as during gene therapy procedures. The current
 XX sequence is that of the C-terminal albumin-(GGS)4GG-DX-890 fusion DNA of
 XX the invention.
 XX
 XX SQ Sequence 1965 BP; 586 A; 383 C; 469 G; 527 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 2.32e-35 Length: 1965
 XX Score: 329.00 Matches: 56
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 10 Gaps: 0
 XX
 XX US-10-038-722-27 (1-56) x ADF42043 (1-1965)

```

QY      1  GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB      1798  GAAGCCTGTAACCTGCAATGTTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 1857
QY      21  PheAspAlaValIlyGlyLylsCyValLeuPheProTyrgIyGlyCyGlnGlyAsnGly 40
DB      1858  TTCGATGCTGTTAAGGTAAGTGTGTTGTTCCATATGGGTGGTTCAGAGTAACGGT 1917
QY      41  AsnLysPheTyrsSerGluLylsGlyCysArgGluTyrgCysGlyValPro 56
DB      1918  AACCAAGTCTACTCTGAAAAGGAATGTAGAGAAATCTGTGGTGTCCA 1965

RESULT 11
ID      ADF42041
AC      ADF42041 standard; DNA, 1965 BP.
XX
XX      12-FEB-2004 (first entry)
DE      N-terminal DX-890-(GGG)4GG-albumin fusion DNA.
XX
XX      albumin fusion; Kunitz domain; cytosstatic; haemostatic;
KW      hereditary angioedema; cancer; bleeding; gene therapy;
KW      N-terminal DX-890-(GGG)4GG-albumin fusion; ds; gene.
XX
XX      Synthetic.
OS      Unidentified.

XX      Key      Location/Qualifiers
FH      1..1965
FT      CDS
FT      /*tag= a
FT      /partial
FT      /product= "N-terminal DX-890-(GGG)4GG-albumin fusion
FT      /protein"
FT      /note= "No start or stop codon"
XX
XX      WO2003066824-A2.
XX
XX      14-AUG-2003.
XX
XX      07-FEB-2003; 2003WO-US003616.
XX
XX      07-FEB-2002; 2002US-0355547P.
XX
XX      (AVET ) AVENTIS BEHRING GMBH.
XX      (AVET ) AVENTIS BEHRING LLC.
XX      (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX      (DYAX-) DYAX CORP.
XX
XX      Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI      Ley AC;
XX
XX      WPI; 2003-731497/69.
XX      P-PSDB; ADF42042.
XX
XX      Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT      useful for preparing a composition for treating a patient with hereditary
PT      angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX      Example 23; Page 74; 110pp; English.
XX
XX      The invention relates to a novel albumin fusion protein comprising a
XX      Kunitz domain peptide or its fragment or variant and an albumin or its
XX      fragment or variant. The fusion protein of the invention demonstrates
XX      cytosstatic and haemostatic activities and may be useful for preparing a
XX      composition for treating a patient with hereditary angioedema, an
XX      angioedema-related disease, cancer, a cancer-related disease or a
XX      bleeding disorder, as well as during gene therapy procedures. The current
XX      sequence is that of the N-terminal DX-890-(GGG)4GG-albumin fusion DNA of
XX      the invention.
XX
XX      Sequence 1965 BP; 540 A; 386 C; 477 G; 562 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 2.32e-35
Score: 329.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Gaps: 0

US-10-038-722-27 (1-56) x ADF42041 (1-1965)

QY      1  GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB      1  GAAGCCTGTAACCTGCAATGTTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 60
QY      21  PheAspAlaValIlyGlyLylsCyValLeuPheProTyrgIyGlyCyGlnGlyAsnGly 40
DB      61  TTCGATGCTGTTAAGGTAAGTGTGTTGTTCCATATGGGTGGTTCAGAGTAACGGT 120
QY      41  AsnLysPheTyrsSerGluLylsGlyCysArgGluTyrgCysGlyValPro 56
DB      121  AACCAAGTCTACTCTGAAAAGGAATGTAGAGAAATCTGTGGTGTCCA 168

RESULT 12
ID      ADR90035
AC      ADR90035 standard; DNA, 1965 BP.
XX
XX      18-NOV-2004 (first entry)
DE      C-terminal DX-890-(GGG)4 GG-albumin fusion DNA.
XX
XX      Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW      hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW      asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW      cytosstatic; haemostatic; chimeric; DX-890; human albumin; HA; human;
XX      gene; ds.
XX
XX      Homo sapiens.
OS      Chimeric.
OS      Unidentified.

XX      Key      Location/Qualifiers
FH      1..1965
FT      CDS
FT      /*tag= a
FT      /product= "C-terminal DX-890-(GGG)4 GG-albumin fusion
FT      /protein"
FT      /partial
FT      /note= "No start and stop codon"
XX
XX      US2004171794-A1.
XX
XX      02-SEP-2004.
XX
XX      07-FEB-2003; 2003US-00361997.
XX
XX      07-FEB-2003; 2003US-00361997.
XX
XX      (LADN/) LADNER R C.
XX      (LEYA/) LEY A C.
XX
XX      Ladner RC, Ley AC;
PI
XX
XX      WPI; 2004-625120/60.
XX      P-PSDB; ADR90036.
XX
XX      New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT      for the treatment of e.g. cystic fibrosis and related disease.
XX
XX      Example 9; SEQ ID NO 60; 123pp; English.
XX
XX      The invention relates to proteins comprising kunitz domain peptide,
CC

```

CC designated Dpi-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cystostatic and haemostatic agent. The present sequence is a C-terminal DX
 CC -890-(GGS)4 GG-albumin fusion DNA. This fusion DNA contains DX-890 cDNA,
 CC GS linker region and human albumin (HA). This sequence is used in the
 CC exemplification of the invention.

XX SQ Sequence 1965 BP; 586 A; 383 C; 469 G; 527 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,32e-35	Length:	1965
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90035 (1-1965)

QY 1 GUAAGCYAAsnleuprollevalargglyProCysillealphepProargTrrpala 20

DB 1798 GAAGCCTGTAACCTCCCAATGTTAGAGGTCATGATTCCTTCCCAAGATGGGCT 1857

QY 21 PheapAlaVallyGlyLyseCyseValleupheProTrrglyGlyCyseGlnGlyAangly 40

DB 1858 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTAAGGTAAAGGCT 1917

QY 41 AsnlySphetyrSerglulysGlyCysArggluTrrCyseGlyValPro 56

DB 1918 AACAACTTACTCTGAAAGAAAGATGAGAAATCTGTGGTTCCTCA 1965

RESULT 13

ADR90033 standard; DNA; 1965 BP.

AC ADR90033;

DT 18-NOV-2004 (first entry)

DE N-terminal DX-890-(GGS)4 GG-albumin fusion DNA.

KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;

KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

KW cystostatic; haemostatic; chimeric; DX-890; human albumin; HA; human;

OS Homo sapiens.

OS Chimeric.

OS Undifferentiated.

OS Key

FT CDS

FT 1.1965

FT /tag= a

FT /product= "N-terminal DX-890-(GGS)4 GG-albumin fusion

FT protein"

FT /partial

FT /note= "No start and stop codon"

XX US2004171794-A1.

XX 02-SEP-2004.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX (LADN/) LADNER R C.

XX (LEVA/) LEY A C.

XX PA

XX PF

PI Ladder RC, Ley AC;

XX WPI; 2004-625120/60.

DR P-PSDB; ADR90034.

XX New kunitz domain peptide useful as human neutrophil elastase inhibitor

PT for the treatment of e.g. cystic fibrosis and related disease.

PS Example 8; SEQ ID NO 58; 123pp; English.

CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated Dpi-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cystostatic and haemostatic agent. The present sequence is a N-terminal DX
 CC -890-(GGS)4 GG-albumin fusion DNA. This fusion DNA contains DX-890 cDNA,
 CC GS linker region and human albumin (HA). This sequence is used in the
 CC exemplification of the invention.

XX SQ Sequence 1965 BP; 540 A; 386 C; 477 G; 562 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,32e-35	Length:	1965
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90033 (1-1965)

QY 1 GUAAGCYAAsnleuprollevalargglyProCysillealphepProargTrrpala 20

DB 1 GAAGCCTGTAACCTCCCAATGTTAGAGGTCATGATTCCTTCCCAAGATGGGCT 60

QY 21 PheapAlaVallyGlyLyseCyseValleupheProTrrglyGlyCyseGlnGlyAangly 40

DB 61 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTAAGGTAAAGGCT 120

QY 41 AsnlySphetyrSerglulysGlyCysArggluTrrCyseGlyValPro 56

DB 121 AACAACTTACTCTGAAAGAAAGATGAGAAATCTGTGGTTCCTCA 168

RESULT 14

ADP42053 standard; DNA; 3255 BP.

AC ADP42053;

DT 12-FEB-2004 (first entry)

DE Plasmid pDB2300X2 NotI modified expression cassette DNA.

KW albumin fusion; Kunitz domain; cytosstatic; haemostatic;

KW hereditary angioedema; cancer; bleeding; gene therapy;

KW plasmid pDB2300X2 NotI expression cassette; ds; gene; DX-890.

OS Synthetic.

OS Undifferentiated.

OS Key

FT CDS

FT 829.2913

FT /tag= a

FT /product= "Plasmid pDB2300X2 NotI modified expression

FT cassette protein"

XX MO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING LLC.
PA (DEL2) DELTA BIOTECHNOLOGY LTD.
XX (DYAX-) DYAX CORP.
XX
PI Hauser H, Welmer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
XX
XX WPI; 2003-731497/69.
DR P-PSDB; ADF42054.
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
XX angiodema or angiodema-related disease, cancer or bleeding disorder.
XX
PS Example 23; Page 85-89; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angiodema, an
CC angiodema-related disease, cancer, a cancer-related disease, or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related plasmid PDB2300X2
CC modified NotI expression cassette DNA of the invention which has N-
CC terminal DX-890 and C-terminal linker ready for a second DX-890 sequence.
XX
SQ Sequence 3255 BP; 931 A; 666 C; 769 G; 889 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,486-35 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42053 (1-3255)
OY 1 GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 901 GAAGCCTGTAAGCTTGTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 960
OY 21 PheAspAlaValIleGlyLysCySValIleuPheProTyGlyGlyCySgInGlyAsnGly 40
DB 961 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGAGTGCTTGTCAAGGTAAACGT 1020
OY 41 AsnLysPheTyRSeGluLysGlyCysArgGlyTrpCySgIlyValPro 56
DB 1021 AACAGTCTACTCTGAAGAAAGATGAGATGACTGTGGTTCACA 1068
XX
RESULT 15
ADR90045
ID ADR90045 standard; DNA; 3255 BP.
XX
XX ADR90045;
AC
XX 18-NOV-2004 (first entry)
DT
XX
DE PDB2300X2-2xGS linker fusion DNA.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angiodema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytosolic; haemostatic; chimeric; human; rRNA synthase gene;
KW human albumin; Ha; gene; ds.
XX
XX Homo sapiens.
OS
OS Chimeric.

OS Unidentified.
XX
XX Key Location/Qualifiers
FH CDS 829..2916
FT
FT
FT /tag= b
FT /product= "pDB2300X2-2xGS linker fusion protein"
FT /note= "CDS contains two stop codons"
FT sig_peptide 829..900
FT /tag= a
FT mat_peptide 901..2910
FT /tag= d
FT /product= "Mature pDB2300X2-2xGS linker fusion protein"
FT /note= 901..1068
FT misc_feature 1069..1110
FT /tag= c
FT /note= "DX-890 DNA"
FT misc_feature 1111..1285
FT /tag= e
FT /note= "GS-linker region DNA"
FT misc_feature 1111..1285
FT /tag= f
FT /note= "rRNA gene"
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
XX Ladner RC, Ley AC;
XX WPI; 2004-625120/60.
XX P-PSDB; ADR90046.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 18; SEQ ID NO 70; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angiodema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytosolic and haemostatic agent. The present sequence is a PDB2300X2-
CC 2xGS linker fusion DNA. This chimeric DNA contains DX-890 cDNA at its N-
CC terminal end, rRNA synthase gene and the linkers at its C-terminal end.
CC This sequence is used in the exemplification of the invention.
XX
SQ Sequence 3255 BP; 931 A; 666 C; 769 G; 889 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,486-35 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADR90045 (1-3255)
OY 1 GluAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 901 GAAGCCTGTAAGCTTGTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 960
OY 21 PheAspAlaValIleGlyLysCySValIleuPheProTyGlyGlyCySgInGlyAsnGly 40
DB 961 TTCGATGCTGTAAAGGTAAGTGTGTTTGTCCCATATGAGTGCTTGTCAAGGTAAACGT 1020

OY 41 AsnlySpheTYrSerGIuLYsGIuCYsArGIuTYrCYsGIyValPro 56
|||||
DB 1021 AACAGTCTACTCTGAAAGAAATGTAGAGAAATCTGTGCTTCCA 1068
RESULT 16
ID ADR90048
XX ADR90048 standard; DNA; 3440 BP.
AC ADR90048;
XX
XX 18-NOV-2004 (first entry)
DE PDB2300X3-2XDX-890 fusion DNA.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cystostatic; haemostatic; chimeric; human; rRNA synthase gene;
KW human albumin; HA; DX-890; gene; ds.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
XX
FH Key
FT CDS 829..3090
FT Location/Qualifiers
FT /tag= b
FT /product= "PDB2300X3-2XDX-890 fusion protein"
FT /note= "CDS contains two stop codons"
FT 829..900
FT /tag= a
FT 901..3084
FT /tag= d
FT /product= "ature PDB2300X2-2XGS linker fusion protein"
FT 901..1068
FT /tag= c
FT /note= "DX-890 DNA #1"
FT 1069..1110
FT /tag= e
FT /note= "GS-linker region DNA"
FT 1111..2865
FT /tag= f
FT /note= "rHA gene"
FT 2866..2901
FT /tag= g
FT /note= "GS-linker region DNA"
FT 2902..3084
FT /tag= h
FT /note= "DX-890 DNA #2"
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
XX LADNER RC, LEY AC;
XX
XX WPI; 2004-625120/60.
XX P-PSDB; ADR90049, ADR90050.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 19; SEQ ID NO 73; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,

CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cystostatic and haemostatic agent. The present sequence is a PDB2300X3-
CC 2XDX-890 fusion DNA. This chimeric DNA contains two DX-890 CDNA's, rHA
CC synthase gene and the linkers. This sequence is used in the
XX exemplification of the invention.
SQ Sequence 3440 BP; 966 A; 711 C; 820 G; 943 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4,81e-35 Length: 3440
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-038-722-27 (1-56) x ADR90048 (1-3440)
OY 1 GIuAlaCYsAenLeuProIleValArgGIyProCYsIleAlaPhePheProArGTrPa1a 20
|||||
DB 901 GAAGCTGTACTGTGCAATGTGTAGAGTCCATGTATGCTTCTTCCCAAGATGGGCT 960
OY 21 PheAePAIValLYsGIuLYsCYsValLeuPheProTYrGIyGIyCYsGIInGIyAAsGIY 40
|||||
DB 961 TTCATGCTGTTAAGGTGAAGTGTGTTTGTTCCTATGTGTGTGTGTGTCAAGTACCGT 1020
OY 41 AsnlySpheTYrSerGIuLYsGIuCYsArGIuTYrCYsGIyValPro 56
|||||
DB 1021 AACAGTCTACTCTGAAAGAAATGTAGAGAAATCTGTGCTTCCA 1068
RESULT 17
ADP42056
ID ADP42056 standard; DNA; 3441 BP.
XX
XX ADP42056;
XX
XX 12-FEB-2004 (first entry)
XX
XX Plasmid PDB2300X3 NctI modified expression cassette DNA - 2X DX-890.
XX
XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy;
KW plasmid PDB2300X3 NctI expression cassette; ds; gene; DX-890.
XX
XX Synthetic.
OS Unidentified.
OS
FH Key
FT CDS 829..3087
FT Location/Qualifiers
FT /tag= a
FT /product= "Plasmid PDB2300X3 NctI modified expression
FT cassette protein - 2X DX-890"
XX
XX MO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVENT) AVENTIS BEHRING GMBH.
XX (AVENT) AVENTIS BEHRING LLC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (DVAX-) DVAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
XX

DR WPI; 2003-731497/69.
DR P-PSDB; ADF42057.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angiodema or angiodema-related disease, cancer or bleeding disorder.
XX
PS Example 23; Page 90-94; 110pp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cyostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angiodema, an
CC angiodema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related plasmid PDB2300X3
CC modified NotI expression cassette DNA of the invention which has 2 DX-890
CC sequences.
XX
SQ Sequence 3441 BP; 966 A; 711 C; 820 G; 944 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.81e-35 Length: 3441
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42056 (1-3441)
XX
QY 1 GIUAlaCyseAnleuProIleValaArgGlyProCyseIleAlaPhePheProArgTrpAla 20
Db 901 GAGGCTTGAATCTTCCATGTGTAGAGGTCATGTATGCTTTCTCCCAAGATGGGCT 960
QY 21 PheaSPAlaValAllyeGlyLyeCyseValleuPheProTyrglyGlyCyseGlnGlyVaangly 40
Db 961 TTCATGCTGTAAAGGTAAGTGTGTTTGTTCCTATGCGTGTGTCAGAGTAACGGT 1020
QY 41 AenlySPheTySerGluLylGlyCyseArgGlyLylTyrglyValPro 56
Db 1021 AACAGTCTACTCTGAAAGGAATGTAGAGATATCTGGGTCCA 1068
XX
RESULT 18
ADFA2068 standard; DNA; 3444 BP.
XX
AC ADF42068;
XX
XX 12-FEB-2004 (first entry)
XX
DE Plasmid pDB2301X-derived DPI-14-(GGS) 4GG-rHA-(GGS) 4GG-DX-890 fusion DNA.
XX
KW albumin fusion; Kunitz domain; cyostatic; haemostatic;
KW hereditary angiodema; cancer; bleeding; gene therapy; plasmid PDB2301X;
KW ds; DPI-14-(GGS) 4GG-rHA-(GGS) 4GG-DX-890 fusion; gene.
XX
XX Synthetic.
OS Unidentified.
OS
XX
FH Key Location/Qualifiers
FT CDS 829..3090
FT
FT /*tag= a
FT /product= "Plasmid pDB2301X-derived DPI-14-(GGS) 4GG-rHA-
FT (GGS) 4GG-DX-890 fusion precursor protein"
XX
XX MO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX

PR 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING LLC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
PI
XX
DR WPI; 2003-731497/69.
DR P-PSDB; ADF42028.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angiodema or angiodema-related disease, cancer or bleeding disorder.
XX
PS Example 22; Page 66-68; 110pp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates a
CC cyostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angiodema, an
CC angiodema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the plasmid PDB2301X-derived DPI-14-(GGS) 4GG-rHA-
CC (GGS) 4GG-DX-890 fusion DNA of the invention. NOTE: This sequence also
CC contains regions of cDNA.
XX
SQ Sequence 3444 BP; 968 A; 713 C; 819 G; 944 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.82e-35 Length: 3444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42068 (1-3444)
XX
QY 1 GIUAlaCyseAnleuProIleValaArgGlyProCyseIleAlaPhePheProArgTrpAla 20
Db 2920 GAGGCTTGAATCTTCCATGTGTAGAGGTCATGTATGCTTTCTCCCAAGATGGGCT 2979
QY 21 PheaSPAlaValAllyeGlyLyeCyseValleuPheProTyrglyGlyCyseGlnGlyVaangly 40
Db 2980 TTTGACGCGCTCAAGGCAATGCGTCTTTTCTTACGCGGTTGCCAGGCAATGGC 3039
QY 41 AenlySPheTySerGluLylGlyCyseArgGlyLylTyrglyValPro 56
Db 3040 AATAAATTTTATAGCGAAGAAAGAGTCCGTGATGTTCCGGGCTTCC 3087
XX
RESULT 19
ADR90019 standard; DNA; 3444 BP.
XX
AC ADR90019;
XX
XX 18-NOV-2004 (first entry)
XX
DE DPI-14-(GGS) 4 GG-rHA-(GGS) 4 GG-DX-890 fusion DNA.
XX
KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angiodema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cyostatic; haemostatic; human; rHA synthase gene; human albumin; HA;
KW DPI-14; DX-890; chimeric; gene; ds.
XX
XX Homo sapiens.
OS Chimeric.
OS Unidentified.
OS

XX	Key	Location/Qualifiers
FH	CDS	829..3090
FT		/tag= b
FT		/product= "DPI-14-(GGG) 4 GG-rHA-(GGG) 4 GG-DX-890 fusion protein"
FT	sig_peptide	829..900
FT		/tag= a
FT		/note= "Fusion leader sequence"
FT	CDS	901..3090
FT		/tag= d
FT		/product= "Mature DPI-14-(GGG) 4 GG-rHA-(GGG) 4 GG-DX-890 fusion protein"
FT	misc_feature	901..1080
FT		/tag= c
FT		/note= "DPI-14 CDNA"
FT		1081..1121
FT	misc_feature	/tag= e
FT		/note= "GS linker region"
FT		1122..2877
FT		/tag= f
FT	misc_feature	/note= "rHA synthase gene"
FT		2878..2918
FT		/tag= g
FT		/note= "GS linker region"
FT		2919..3087
FT		/tag= h
FT		/note= "DX-890 DNA"
XX		
FN	US2004171794-A1.	
PD	02-SEP-2004.	
PE	07-FEB-2003; 2003US-00361997.	
PR	07-FEB-2003; 2003US-00361997.	
PA	(LADN/) LADNER R C. (LEYA/) LEY A C.	
PI	Ladner RC, Ley AC;	
DR	WPI, 2004-625120/60.	
DR	P-PsDB; ADR90020, ADR90021.	
PT	New kunitz domain peptide useful as human neutrophil elastase inhibitor for the treatment of e.g. cystic fibrosis and related disease.	
PS	Example 22; SEQ ID NO 44; 123pp; English.	
CC	The invention relates to proteins comprising kunitz domain peptide, designated DPI-14 for inhibiting human neutrophil elastase, fused to albumin. The invention is useful for treating cystic fibrosis and related diseases, hereditary angioedema, cancer and related diseases including chronic obstructive pulmonary disease, asthma, bronchitis, acute respiratory syndrome, pneumonia and bleeding. The invention acts as a cytoskeletal and haemostatic agent. The present sequence is a DPI-14-(GGG) 4 GG-rHA-(GGG) 4 GG-DX-890 fusion DNA. This fusion DNA contains DPI-14 CDNA, GS linker region, rHA (human albumin) synthase gene and DX-890 CDNA. This sequence is used in the exemplification of the invention.	
SO	Sequence 3444 BP; 968 A; 713 C; 819 G; 944 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	4, 82e-35	Length: 3444
Score:	329.00	Matches: 56
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	13	Gaps: 0

US-10-038-722-27 (1-56) x ADR90019 (1-3444)

Oy	1	Glul1a1CyAsnLeuProIleValAlaArg1yProCysIleAlaPhePheProArGtrPa1a	20
Dd	2920	GAGCGTTCGCAATCTTCATGCTGCGGCGCCCTTGATCGCTTTTCTTCGTTGGCC	297
Oy	21	PheAspAlaVal1yLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly	40
Dd	2980	TTTGACGCGCGTCGCAAGGCAATGGTGCTCTTTTCTTACGCGCGGTGCGAGGCAATGCG	303
Oy	41	AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
Dd	3040	AATAAATTTTATGCGAGAAAGAGCGCGTGTAGATATGCGGCGCTCCT	3087
RESULT 20			
AT35166			
ID	AA135166	standard; DNA; 8584 BP.	
XX	AA135166;		
XX	14-FEB-1997	(first entry)	
DT			
XX			
DE	Plasmid pHL-D2 (MAlphaPrePro: EPI-HNE-3).		
XX			
XX	Aprotinin; Kunitz domain; human neutrophil elastase; hNE;		
KW	connective tissue; alpha 1 protease inhibitor; API; neutrophil;		
KW	alpha antitrypsin; respiratory disorder; cystic fibrosis;		
KM	smokers emphysema; ds.		
XX			
XX	Synthetic.		
OS			
XX			
FH	Key	Location/Qualifiers	
FT	CDS	954..1379	
FT		/*tag= a	
FT		/product= "EPI-HNE-3 modified Kunitz domain"	
XX			
PN	MO9620278-A2.		
PD	04-JUL-1996.		
XX			
PF	15-DEC-1995;	95WO-US016349.	
XX			
PR	16-DEC-1994;	94US-00358160.	
XX			
PA	(PROT-) PROTEIN ENG CORP.		
PI	Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;		
DR	WPI, 1996-321851/32.		
XX			
PT	New engineered inhibitors of human neutrophil elastase - contg. aprotinin		
PT	-like Kunitz domain for treating, e.g. cystic fibrosis or other		
PT	respiratory disorders.		
PS	Example 10; Page 68-73; 105pp; English.		
XX			
CC	Genetically engineered human derived Kunitz domains can be used to		
CC	inhibit human neutrophil elastase, an enzyme involved in the elimination		
CC	of pathogens and the restructuring of connective tissue. In cases of		
CC	reduction of the circulating alpha-1-protease inhibitor (API or alpha1		
CC	antitrypsin), or the inactivation of API by oxidation (smokers		
CC	emphysema), extensive destruction of the lung tissue may result from		
CC	uncontrolled elastolytic activity of human neutrophil elastase. Other		
CC	respiratory disorders such as cystic fibrosis are thought to be caused by		
CC	human neutrophil elastase release by neutrophils. The genetically		
CC	engineered human derived Kunitz domains can be used to treat such		
CC	respiratory disorders. See AA899146-R89211. Fusion genes were used in the		
CC	production of the Kunitz domain derivatives. Protein expression cassettes		
CC	are then cloned into the plasmid pHL-D2 using BamBI and EcoRI		
CC	restriction sites. The cloned sequence is under the transcriptional		
CC	control of Pichia pastoris axo1 gene promoter and regulatory sequences		
CC	and downstream polyadenylation and transcription termination sequences.		
CC	Transformed strains of P. pastoris were used to express the various Epi-		
CC	HNE proteins derived from the BPT and ITI-D2 Kunitz domains. This		
CC	sequence comprises pHL-D2 having an EPI-HNE-3 Kunitz domain expression		

CC cassette inserted into it. It was designated PHIL-D2 (MfalpaphPrePro::Epi-
CC HNE-3)
XX
SQ Sequence 8584 BP; 2264 A; 2024 C; 1976 G; 2320 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7,86e-34 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT35166 (1-8584)
QY 2 AlaCysaenLeuProIleValaIArgGlyProCysIleAlaPhePheProArgTTPAlaPhe 21
Db 1212 GCTGTACTGTCATCGTCAGAGGTCATGTCATGCTTCTTCCCAAGATGGGCTTTC 1271
QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyVal 41
Db 1272 GACGCTGTTAGGGGTAAGTGCGCTTGTTCCTCATACGGGTGGTGTGTCAGATACGGGTAC 1331
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1332 AAGTCTACTCTGAGAGAGAGGTAGAGAGTACTGTGTTC 1376
RESULT 21
AAT35168 ID AAT35168 standard; DNA; 8590 BP.
XX AC AAT35168;
XX DT 14-FEB-1997 (first entry)
XX DE Plasmid pD2pick (MfalpaphPrePro::Epi-HNE-3).
XX KM Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
XX KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
XX KM alpha 1 antitrypsin; respiratory disorder; cystic fibrosis;
XX KM smokers emphysema; ds.
XX OS Synthetic.
XX FT Key Location/Qualifiers
FT CDS 954..1379
FT /tag= a
FT /product= "Epi-HNE-3 modified Kunitz domain"
XX PN MO9620278-A2.
XX PD 04-JUL-1996.
XX PF 15-DEC-1995; 95WO-US016349.
XX PR 16-DEC-1994; 94US-00358160.
XX PA (PROT-) PROTEIN ENG CORP.
XX PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX DR WPI; 1996-321851/32.
XX DR P-PSDB; AAR9214.
XX PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
XX PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
XX PT respiratory disorders.
XX PS Example 10; Page 76-81; 105BP; English.
XX CC Genetically engineered human derived Kunitz domains can be used to
XX CC inhibit human neutrophil elastase, an enzyme involved in the elimination
XX CC of pathogens and the restructuring of connective tissue. In cases of

CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR9146-R9211. Fusion genes were used in the
CC production of the Kunitz domain derivatives. Protein expression cassettes
CC are then cloned into the plasmid PHIL-D2 using BamBI and EcoRI
CC restriction sites. The cloned sequence is under the transcriptional
CC control of Pichia pastoris axol gene promoter and regulatory sequences
CC and downstream polyadenylation and transcription termination sequences.
CC Transformed strains of P. pastoris were used to express the various Epi-
CC HNE proteins derived from the BPI and IPI-D2 Kunitz domains. This
CC sequence comprises PHIL-D2 having an Epi-HNE-3 Kunitz domain expression
CC cassette inserted into it. It was designated pD2pick (MfalpaphPrePro::Epi-
CC HNE-3). This sequence differs from the sequence given in AAT35166 by
CC having had two restriction sites, one BamBI and one AatII site, removed
CC from the sequence. This means that the Kunitz domain encoding segment is
CC bounded by unique AatII and EcoRI sites
SQ Sequence 8590 BP; 2265 A; 2026 C; 1972 G; 2321 T; 0 U; 6 Other;
Alignment Scores:
Pred. No.: 7,87e-34 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT35166 (1-8590)
QY 2 AlaCysaenLeuProIleValaIArgGlyProCysIleAlaPhePheProArgTTPAlaPhe 21
Db 1212 GCTGTACTGTCATCGTCAGAGGTCATGTCATGCTTCTTCCCAAGATGGGCTTTC 1271
QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyVal 41
Db 1272 GACGCTGTTAGGGGTAAGTGCGCTTGTTCCTCATACGGGTGGTGTGTCAGATACGGGTAC 1331
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1332 AAGTCTACTCTGAGAGAGAGGTAGAGAGTACTGTGTTC 1376
RESULT 22
AAT79078 ID AAT79078 standard; DNA; 204 BP.
XX AC AAT79078;
XX DT 11-NOV-1997 (first entry)
XX DE Anti-trypsin inhibitor UTI Kunitz domain 2 coding sequence.
XX KM Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX KM neutrophil; disease; modification; site directed mutagenesis; ss.
XX OS Homo sapiens.
XX PN JP09124700-A.
XX PD 13-MAY-1997.
XX PF 07-NOV-1995; 95JP-00288527.
XX PR 07-NOV-1995; 95JP-00288527.
XX PA (GREC) GREEN CROSS CORP.
XX DR WPI; 1997-316576/29.
XX DR P-PSDB; AAW25930.

XX New protease inhibitor - useful for treating diseases involving elastase.
PT Disclosure; Page 24; 37pp; Japanese.
PS
XX
XX This is the nucleotide sequence encoding the anti-trypsin inhibitor UTI
CC Kunitz domain 2. The nucleotide sequence was used to construct a novel
CC protease inhibitor in which the active site residues of the Kunitz domain
CC 1 (M5929) are substituted (see AAT79080, AAT79081 and AAT79083). The
CC modified protease inhibitors are targeted to the protease elastase,
CC especially from neutrophils and can be used to treat diseases associated
CC with elastase. Modifications of the active site were done by site
CC directed mutagenesis
SQ
XX Sequence 204 BP; 37 A; 56 C; 67 G; 44 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.7e-32 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT79078 (1-204)
QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 10 GCATGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 69
QY 22 AspAlaValIleGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAAGGGAAGTGGCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGGGGTGTCCCT 174
RESULT 23
AAV40045
ID AAV40045 standard; cDNA to mRNA; 204 BP.
AC AAV40045;
DT 09-NOV-1998 (first entry)
DE UTI cDNA SEQ ID NO:27 from WO9829453 Example 13.
KW Drug; cell membrane-directed drug; phospholipid; lipid bilayer;
KW cell cortex; blood coagulation; inflammation; immunological disorder; ss.
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..204
FT CDS /*tag= a
FT /note= "no stop codon given"
XX
XX WO9829453-A1.
XX
XX 09-JUL-1998.
XX
XX 05-JAN-1998; 98WO-JP000002.
XX
XX 27-DEC-1996; 96JP-00359053.
XX
XX (MOCH) MOCHIDA PHARM CO LTD.
XX
XX Kuriyama S, Hasegawa T;
XX
XX WPI; 1998-388051/33.
XX
XX P-PSDB; AAM69521.
XX

XX
PT Drugs containing peptide(s) with specific affinity to phospholipid(s) -
PT such as phosphatidyl serine, for treatment of blood coagulation,
PT inflammatory and immunological disorders.
PS
XX
XX Example 13; Page 83; 117pp; Japanese.
XX
XX The present invention describes drug compositions which contain as an
CC active component a peptide which has specific affinity to particular
CC phospholipids (such as phosphatidyl ethanolamine or phosphatidyl serine),
CC especially to phospholipid which constitute a lipid bilayer of cellular
CC cortex and of which the concentration in the bilayer increases in cells
CC which are abnormal (e.g. through injury, denaturation or activation). In
CC particular, the peptide contains a sequence having phospholipid affinity
CC and a structure of formula (I): (A1)a-(A2)b-(A3)c, where (A1) is one of
CC two specific sequences (see AAM69516 and AAM69519), (A2) and (A3) are
CC TRVRIHPSQSWHQIALR, LRVIRHPSQSWHQIALR (see AAM69517) or MEVLGCEAQNLY
CC (see AAM69518); a = 0-5; b = 1-5, and c = 0-5. Preferred are the formulae
CC A1-A2-A3, A2-A2-A3, A2-A2-A2-A3 or A2-A2 (especially A2-A2-A3, A2-
CC A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a blood
CC factor, especially thrombo-modulin, urina-statin or membrane cofactor
CC protein. The drugs are used for the treatment and prevention of diseases
CC involving blood coagulation, inflammatory and immunological disorders.
CC The present sequence encodes a protein from the present invention
SQ
XX
XX Sequence 204 BP; 37 A; 59 C; 65 G; 43 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.7e-32 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAV40045 (1-204)
QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 4 GCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 63
QY 22 AspAlaValIleGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 64 GATGCTGTCAAGGGAAGTGGCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 123
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 124 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGGGGTGTCCCT 168
RESULT 24
AAQ78607
ID AAQ78607 standard; DNA; 210 BP.
AC AAQ78607;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE DNA sequence downstream of DNA encoding E. coli alkaline phosphatase.
KW fusion protein; protein expression; secretion; alkaline phosphatase;
KW recombinant DNA technology; signal peptide; Escherichia coli; ss.
XX Synthetic.
OS
XX
XX EP624644-A1.
XX
XX 17-NOV-1994.
XX
XX 29-APR-1994; 94EP-00106773.
XX
XX 01-MAY-1993; 93JP-00128528.
XX
XX

PA (MOCH) MOCHIDA PHARM CO LTD.
 XX Morishita H, Kanamori T, Nobuhara M;
 XX WPI: 1994-350784/44.
 DR P-PSDB; AAR65481.
 XX
 PT Vector contg. a DNA fragment - used to produce a protein of interest.
 PS
 XX Example 3; Page 15; 65bp; English.
 XX
 CC AAQ78607 is a nucleotide sequence which is downstream of a nucleotide
 CC sequence that encodes E. coli alkaline phosphatase signal peptide. It
 CC encodes the protein shown in AAR65476. Plasmid pMS94, used for the
 CC expression of AN68 (sic) (see AAR65478), was constructed from plasmid
 CC pMS52 which contains a tryptophan promoter, a Kanamycin resistant gene
 CC and also AAQ78607. The vectors for the expression of AN68, each contain a
 CC nucleotide sequence of general formula: j-x-y-z (j = AAQ78606; x =
 CC AAQ78598/078601; y = a nucleotide sequence that encodes Met; and z
 CC represents the nucleotide sequence that encodes AN68). When a protein of
 CC interest is expressed as a fusion protein contg. 'x' (encoded by x) its
 CC expression and/or secretion quantity increases. (Updated on 25-MAR-2003
 CC to correct PN field.)
 CC
 SQ Sequence 210 BP; 38 A; 63 C; 65 G; 44 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 4,88e-32 Length: 210
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 2 Gaps: 0
 US-10-038-722-27 (1-56) x AAQ78607 (1-210)
 QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 10 GCCTGCATCTCTCCCATAGTCCGGGGCCCTCCGAGCTTATCATCAGCTCTGGGCAATT 69
 QY 22 AspAlaValAllyGlyLysCyValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 70 GATGCTGTCAAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCACAGGGAACCGGAAC 129
 QY 42 LysPheTyrSerGlyLysGlyLysArgGlyLysTyrCysGlyValPro 56
 DB 130 AAGTTCTACTCAGAGAAGGAGTGCAGAGTACTGCGGTGCTCT 174
 RESULT 25
 ID AAQ64758 standard; DNA; 210 BP.
 XX
 AC AAQ64758;
 XX
 DT 10-MAR-2003 (revised)
 DT 27-JUN-1994 (first entry)
 XX
 DE Protease inhibitor gene #3.
 XX
 KW Protease inhibitor; core region; dyspnea disease of adult; allergy;
 KW polycystic failure; shock; pancreatitis; chronic articular rheumatism;
 KW intravascular coagulation disease; operation invasion; arthritis; se.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FH misc_feature 1..9
 FT /tag= a
 FT /note= "May be serially deleted by multiples of 3 bp"
 FT misc_feature 13..165
 FT /tag= b
 FT /note= "Wild type core region"

FT misc_feature 169..210
 FT /tag= c
 FT /note= "May be serially deleted by multiples of 3 bp"
 XX
 XX JP05308988-A.
 XX
 XX 22-NOV-1993.
 XX PD
 XX 12-MAY-1992; 92JP-00146587.
 XX PF
 XX 12-MAY-1992; 92JP-00146587.
 XX PR
 XX 12-MAY-1992; 92JP-00146587.
 XX
 PA (MOCH) MOCHIDA PHARM CO LTD.
 XX
 DR WPI: 1994-002180/01.
 DR P-PSDB; AAR54721.
 XX
 PT New polypeptide - useful for prevention and therapy of diseases related
 PT to protease e.g. pancreatitis.
 XX
 PS Claim 11 and 12; Page 3; 27pp; Japanese.
 XX
 CC The sequences given in AAQ64756-59 are DNA sequences encoding extended
 CC versions of a wild type core polypeptide which acts as a protease
 CC inhibitor. The peptides encoded by these sequences may also contain
 CC deletions within the core region (see also AAQ64751-55). These deletions
 CC lead to the production of peptides with enhanced protease inhibitor
 CC action. These peptides may be used for the prevention and therapy of
 CC diseases related to protease, such as operation invasion, polycystic
 CC failure, shock, pancreatitis, intravascular coagulation disease, dyspnea
 CC disease of adult, chronic articular rheumatism, arthritis or allergy.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 CC
 SQ Sequence 210 BP; 40 A; 60 C; 65 G; 45 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 4,88e-32 Length: 210
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 2 Gaps: 0
 US-10-038-722-27 (1-56) x AAQ64758 (1-210)
 QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 10 GCCTGTAACTTACCAATAGTCCGGGGCCCTCCGAGCTTATCATCAGCTCTGGGCAATT 69
 QY 22 AspAlaValAllyGlyLysCyValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 70 GATGCTGTCAAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCACAGGGAACCGGAAC 129
 QY 42 LysPheTyrSerGlyLysGlyLysArgGlyLysTyrCysGlyValPro 56
 DB 130 AAGTTCTACTCAGAGAAGGAGTGCAGAGTACTGCGGTGCTCT 174

Search completed: February 23, 2005, 04:36:01
 Job time : 395 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: February 23, 2005, 03:27:40 ; Search time 63 Seconds

(without alignments)
290.881 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPYRGPCIAFFPRWA.....QGNNGKFKYSEKREYCGVP 56

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	329	100.0	56 14 US-10-038-722-27 = L L F F U	Sequence 27, Appl
2	329	100.0	56 15 US-10-456-986A-49 = L L F F U	Sequence 49, Appl
3	329	100.0	56 16 US-10-361-997-40 = L L	Sequence 40, Appl
4	329	100.0	141 14 US-10-038-722-27	Sequence 74, Appl
5	329	100.0	655 16 US-10-361-997-59	Sequence 59, Appl
6	329	100.0	655 16 US-10-361-997-61	Sequence 61, Appl
7	329	100.0	694 16 US-10-361-997-71	Sequence 71, Appl
8	329	100.0	728 16 US-10-361-997-75	Sequence 75, Appl
9	329	100.0	729 16 US-10-361-997-46	Sequence 46, Appl
10	329	100.0	752 16 US-10-361-997-74	Sequence 74, Appl
11	329	100.0	753 16 US-10-361-997-45	Sequence 45, Appl
12	324	98.5	56 14 US-10-038-722-26 = L L F F U	Sequence 26, Appl
13	324	98.5	56 15 US-10-456-986A-47 = L L F F U	Sequence 47, Appl

14	324	98.5	56 15 US-10-456-986A-48 = L L F F U	Sequence 48, Appl
15	324	98.5	141 14 US-10-038-722-72 = L L F F U	Sequence 72, Appl
16	324	98.5	141 14 US-10-038-722-26 = L L F F U	Sequence 76, Appl
17	296	90.0	57 10 US-09-974-026-26 = L L F F U	Sequence 26, Appl
18	296	90.0	57 10 US-10-167-351-78 = L L F F U	Sequence 78, Appl
19	296	90.0	58 14 US-10-038-722-25	Sequence 25, Appl
20	296	90.0	58 15 US-10-456-986A-31	Sequence 28, Appl
21	296	90.0	58 16 US-10-361-997-8	Sequence 31, Appl
22	296	90.0	68 15 US-10-298-796-23	Sequence 8, Appl
23	296	90.0	147 14 US-10-038-722-77	Sequence 23, Appl
24	296	90.0	147 15 US-10-298-796-24	Sequence 77, Appl
25	296	90.0	352 15 US-10-291-172-281	Sequence 24, Appl
26	296	90.0	352 15 US-10-291-265-450	Sequence 281, Appl
27	296	90.0	352 15 US-10-291-265-922	Sequence 450, Appl
28	296	90.0	352 15 US-10-221-278-281	Sequence 922, Appl
29	296	90.0	366 9 US-09-925-301-1175	Sequence 281, Appl
30	294	89.4	58 14 US-10-167-351-131	Sequence 1175, Appl
31	294	89.4	58 16 US-10-361-997-20	Sequence 131, Appl
32	294	89.4	61 10 US-09-896-095-171	Sequence 20, Appl
33	294	89.4	61 14 US-10-038-722-114	Sequence 171, Appl
34	294	89.4	61 15 US-10-115-134-28	Sequence 114, Appl
35	287	87.2	58 14 US-10-167-351-130	Sequence 28, Appl
36	285	86.6	58 14 US-10-167-351-132	Sequence 130, Appl
37	272	82.7	61 10 US-09-896-095-178	Sequence 132, Appl
38	272	82.7	61 14 US-10-038-722-121	Sequence 178, Appl
39	272	82.7	61 15 US-10-115-134-35	Sequence 121, Appl
40	271	82.4	58 14 US-10-167-351-79	Sequence 35, Appl
41	261	79.3	58 14 US-10-167-351-133	Sequence 79, Appl
42	221	67.2	58 14 US-10-038-722-63	Sequence 133, Appl
43	216	65.7	58 14 US-10-038-722-57	Sequence 63, Appl
44	203	61.7	58 14 US-10-038-722-67	Sequence 57, Appl
45	201	61.1	58 14 US-10-038-722-37	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-038-722-27
Sequence 27, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: RT-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Epi-HNE-4
US-10-038-722-27

Query Match 100.0%; Score 329; DB 14; Length 56;
Best local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EACNLPYRGPCIAFFPRWADAVKGCVLPPYGGCQGNKFKYSEKREYCGVP 56

Db 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 2
US-10-456-986A-49
; Sequence 49, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hiran, Shrish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-4 Sequence
US-10-456-986A-49

Query Match 100.0%; Score 329; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 3
US-10-361-997-40
; Sequence 40, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-10-361-997-40

Query Match 100.0%; Score 329; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 4

US-10-038-722-74
; Sequence 74, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BacBI-AccII-EcoRI cassette for expression of Epi-HNE-4 (Table 252
US-10-038-722-74

Query Match 100.0%; Score 329; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 6.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 86 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 5
US-10-361-997-59
; Sequence 59, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the N-terminal
; OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion protein
US-10-361-997-59

Query Match 100.0%; Score 329; DB 16; Length 655;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADFADAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 6
US-10-361-997-61
; Sequence 61, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 61
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the C-terminal
; OTHER INFORMATION: albumin-(GGG)4GG-DX-890 fusion protein
US-10-361-997-61

Query Match 100.0%; Score 329; DB 16; Length 655;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 56
Db 600 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 555

RESULT 7
US-10-361-997-71
; Sequence 71, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoded by NotI cassette of
; OTHER INFORMATION: pDB2300X2 with DX890 (Nterm) and Cterm linker
; OTHER INFORMATION: ready for second DX890
US-10-361-997-71

Query Match 100.0%; Score 329; DB 16; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 56
Db 25 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 80

RESULT 8
US-10-361-997-75
; Sequence 75, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of
; OTHER INFORMATION: DX-890::((GGG)4GG::HA::((GGG)4GG::DX890
US-10-361-997-75

Query Match 100.0%; Score 329; DB 16; Length 728;
Best Local Similarity 100.0%; Pred. No. 3.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 56
Db 1 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 56

RESULT 9
US-10-361-997-46
; Sequence 46, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Secreted product
US-10-361-997-46

Query Match 100.0%; Score 329; DB 16; Length 729;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 56
Db 674 EACNLPYRGPCIAFFPRMADFADAVKGCVLFPYGGCCGNGNKFYSKEKREYCGVP 729

RESULT 10
US-10-361-997-74
; Sequence 74, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 752
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of NotI cassette of pDB2300X3
US-10-361-997-74

Query Match 100.0%; Score 329; DB 16; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.6e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 25 EACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

RESULT 11
US-10-361-997-45
Sequence 45, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 753
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation product of DPl-14 (GGS) 4
US-10-361-997-45

Query Match 100.0%; Score 329; DB 16; Length 753;
Best Local Similarity 100.0%; Pred. No. 3.6e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 638 EACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 753

RESULT 12
US-10-038-722-26
Sequence 26, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/349,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16

NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Epi-HNE-3
US-10-038-722-26

Query Match 98.5%; Score 324; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 13
US-10-456-986A-47
Sequence 47, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: Ley, Arthur C.
APPLICANT: HIRANI, Shirish
APPLICANT: WILLIAMS, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPI-HNE-2 Sequence
US-10-456-986A-47

Query Match 98.5%; Score 324; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 14
US-10-456-986A-48
Sequence 48, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: LEY, Arthur C.
APPLICANT: HIRANI, Shirish
APPLICANT: WILLIAMS, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-3 Sequence
US-10-456-986A-48

Query Match          98.5%; Score 324; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 56
Db 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 15
US-10-038-722-72
; Sequence 72, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; PRIORITY FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid PHIL-D2 (Mfalphaprepro: EPI-HNE-3) (Table 251)
US-10-038-722-72

Query Match          98.5%; Score 324; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 2,8e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 16
US-10-038-722-76
; Sequence 76, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
```

```
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-3 fusion protein (Table 253)
US-10-038-722-76

Query Match          98.5%; Score 324; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 2,8e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 17
US-09-974-026-26
; Sequence 26, Application US/09974026
; Publication No. US20030194398A1
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P
; APPLICANT: Davis, Gary
; APPLICANT: Delaria, Katherine A
; APPLICANT: Christopher, Marlor W
; APPLICANT: Daniel, Miller K
; TITLE OF INVENTION: Human Btkunin
; FILE REFERENCE: 96-223-22
; CURRENT APPLICATION NUMBER: US/09/974,026
; PRIORITY FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/144,428
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: PCT/US97/03894
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 08/725,251
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US 60/019,793
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: US 60/013,106
; PRIOR FILING DATE: 1996-03-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.
US-09-974-026-26

Query Match          90.0%; Score 296; DB 10; Length 57;
Best Local Similarity 92.7%; Pred. No. 3,4e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 56
Db 3 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFYGGCGGNGNKFYSKECREYCGVP 57

RESULT 18
US-10-167-351-78
; Sequence 78, Application US/10167351
; Publication No. US20030165896A1
; GENERAL INFORMATION:
```

APPLICANT: DYAX CORP.
APPLICANT: Markland, William
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
FILE REFERENCE: DYX-007.2P US-4
CURRENT APPLICATION NUMBER: US/10/167,351
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/638,770
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/114,878
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/240,136
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 08/676,124
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: PCT/US95/00298
PRIOR FILING DATE: 1995-01-11
PRIOR APPLICATION NUMBER: 08/208,265
PRIOR FILING DATE: 1994-03-10
PRIOR APPLICATION NUMBER: 08/179,658
PRIOR FILING DATE: 1994-01-11
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-167-351-78

Query Match 90.0%; Score 296; DB 14; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 58

RESULT 19

US-10-038-722-25
Sequence 25, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/949,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-722-25

Query Match 90.0%; Score 296; DB 14; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 58

DB 4 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 58

RESULT 20
US-10-456-986A-31
Sequence 31, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: Ley, Arthur C.
APPLICANT: Hital, Shirlsh
APPLICANT: Williams, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ITI-D2 Sequence
US-10-456-986A-31

Query Match 90.0%; Score 296; DB 15; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 58

RESULT 21

US-10-361-997-8
Sequence 8, Application US/10361997
Publication No. US20040171794A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: LEY, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-361-997-8

Query Match 90.0%; Score 296; DB 16; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRAFDVAVKGCYLFYGGCGGNGNKFYSKEKREYCGVP 58

RESULT 22
US-10-298-796-23
Sequence 23, Application US/10298796
Publication No. US20030220490A1

```

; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-23

Query Match          90.0%; Score 296; DB 15; Length 68;
Best Local Similarity 92.7%; Pred. No. 4e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56

RESULT 23
US-10-038-722-77
; Sequence 77, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: IT1-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-722-77

Query Match          90.0%; Score 296; DB 14; Length 147;
Best Local Similarity 92.7%; Pred. No. 8.7e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 81 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 135

RESULT 24
US-10-298-796-24
; Sequence 24, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
```

```

; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-24

Query Match          90.0%; Score 296; DB 15; Length 147;
Best Local Similarity 92.7%; Pred. No. 8.7e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 81 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 135

RESULT 25
US-10-291-172-281
; Sequence 281, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030228584A1 Nucleic acids and polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 281
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-281

Query Match          90.0%; Score 296; DB 15; Length 352;
Best Local Similarity 92.7%; Pred. No. 2.1e-28;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 286 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 340

Search completed: February 23, 2005, 03:31:47
Job time : 63 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 03:29:45 ; Search time 39 Seconds
(without alignments)
60.358 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPIVRGPCIAPFPFRA.....QGNKFKYSEKREYCGVP 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169943 seqs, 42035171 residues

Total number of hits satisfying chosen parameters: 169943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	55.3	576	US-11-028-058-7	Sequence 7, Appli
2	182	55.3	640	US-11-028-058-5	Sequence 5, Appli
3	176	53.5	571	US-11-028-058-3	Sequence 3, Appli
4	176	53.5	571	US-11-028-058-49	Sequence 49, Appli
5	172	52.3	548	US-11-028-058-11	Sequence 11, Appli
6	155	47.1	763	PCT-US04-42360-1138	Sequence 1138, Ap
7	155	47.1	763	PCT-US04-42360-1362	Sequence 1362, Ap
8	155	47.1	765	PCT-US04-42360-1136	Sequence 1136, Ap
9	155	47.1	765	PCT-US04-42360-1360	Sequence 1360, Ap
10	150	44.6	552	US-11-028-058-9	Sequence 9, Appli
11	146	44.4	547	US-60-647-493-4	Sequence 4, Appli
12	146	44.4	770	US-10-287-436A-471	Sequence 471, App
13	146	44.4	770	US-10-287-436A-1168	Sequence 1168, Ap
14	146	44.4	770	US-10-903-279-2	Sequence 2, Appli
15	146	44.4	772	US-10-450-763-4945	Sequence 4945, A
16	146	44.4	1137	US-10-450-763-4946	Sequence 4946, A
17	144	43.8	195	US-10-495-300-28	Sequence 28, Appli
18	144	43.8	195	US-11-050-926-304	Sequence 304, App
19	144	43.8	252	US-11-050-926-302	Sequence 302, App
20	140	42.6	841	US-10-450-763-50314	Sequence 50314, A
21	139	42.2	59	US-09-700-179B-46	Sequence 46, Appli
22	135	41.0	59	US-09-700-179B-4	Sequence 4, Appli
23	135	41.0	60	US-09-700-179B-51	Sequence 51, Appli
24	135	41.0	83	US-09-700-179B-18	Sequence 18, Appli
25	135	41.0	83	US-09-700-179B-57	Sequence 57, Appli

26	133	40.4	59	US-09-700-179B-2	Sequence 2, Appli
27	133	40.4	83	US-09-700-179B-16	Sequence 16, Appli
28	133	40.4	83	US-09-700-179B-55	Sequence 55, Appli
29	133	40.4	3176	US-10-852-335A-160	Sequence 160, App
30	133	40.4	3176	US-10-287-436A-503	Sequence 503, App
31	133	40.4	3176	US-10-287-436A-1196	Sequence 1196, Ap
32	132	40.1	59	US-09-700-179B-47	Sequence 47, Appli
33	129	39.2	235	US-11-050-926-316	Sequence 316, Appli
34	127	38.6	88	US-10-485-231-26	Sequence 26, Appli
35	126	38.3	62	US-09-700-179B-48	Sequence 48, Appli
36	122	37.1	59	US-09-700-179B-6	Sequence 6, Appli
37	122	37.1	60	US-09-700-179B-53	Sequence 53, Appli
38	122	37.1	83	US-09-700-179B-20	Sequence 20, Appli
39	122	37.1	83	US-09-700-179B-59	Sequence 59, Appli
40	117	35.6	83	US-09-700-179B-65	Sequence 65, Appli
41	115	35.0	130	PCT-US05-02350-369	Sequence 369, App
42	115	35.0	130	US-11-043-770-369	Sequence 369, App
43	115	35.0	164	US-09-999-570A-96	Sequence 96, Appli
44	115	35.0	225	PCT-US05-02350-368	Sequence 368, App
45	115	35.0	225	US-11-043-770-368	Sequence 368, App

ALIGNMENTS

RESULT 1
US-11-028-058-7
Sequence 7, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028.058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369.736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 7
LENGTH: 576
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-7
Query Match 55.3%; Score 182; DB 7; Length 576;
Best Local Similarity 52.7%; Pred. No. 7; Le-16;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
QY 2 ACNLPYVRGPCIAPFPFRAVDVAVKCYLFPYGGCGGNKFKYSEKREYCGVP 56
DB 385 ACSLPALGGPCAKAVAPRAVYNSQTGQCSFYGGCGGNKFKYSEKREYCGVP 439
RESULT 2
US-11-028-058-5
Sequence 5, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028.058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369.736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645

PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 640
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-5

Query Match 53.3%; Score 182; DB 7; Length 640;
Best Local Similarity 52.7%; Pred. No. 7.9e-16;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSEKREYCGVP 56
DB 449 ACSLPALQGPCAKYVPRMAYNSQTGLCQSFVYGGCGGNGNPFESREACBESCPFP 503

RESULT 3
US-11-028-058-3
Sequence 3, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 571
TYPE: PRT
ORGANISM: Mus sp.
US-11-028-058-3

Query Match 53.5%; Score 176; DB 7; Length 571;
Best Local Similarity 51.9%; Pred. No. 4.2e-15;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSEKREYCGVP 56
DB 381 CSLPALQGPCAKYVPRMAYNSQTGLCQSFVYGGCGGNGNPFESREACBESCPFP 434

RESULT 4
US-11-028-058-49
Sequence 49, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 571
TYPE: PRT
ORGANISM: Mus sp.

US-11-028-058-49

Query Match 53.5%; Score 176; DB 7; Length 571;
Best Local Similarity 51.9%; Pred. No. 4.2e-15;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSEKREYCGVP 56
DB 381 CSLPALQGPCAKYVPRMAYNSQTGLCQSFVYGGCGGNGNPFESREACBESCPFP 434

RESULT 5
US-11-028-058-11
Sequence 11, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 548
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-11

Query Match 52.3%; Score 172; DB 7; Length 548;
Best Local Similarity 50.0%; Pred. No. 1.3e-14;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSEKREYCGVP 56
DB 357 DACVLPVAVQPCRGKPRMAYNSPLTQCHPFPVYGGCGGNGNPFESREACBACFPV 412

RESULT 6
PCT-US04-42360-1138
Sequence 1138, Application PC/TUS0442360
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: 60/531,341
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 1138
LENGTH: 763
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NP_057244
DATABASE ENTRY DATE: 2003-10-04
PCT-US04-42360-1138

Query Match 47.1%; Score 155; DB 1; Length 763;
Best Local Similarity 54.9%; Pred. No. 3.1e-12;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSEKREYCGVP 53
DB 357 DACVLPVAVQPCRGKPRMAYNSPLTQCHPFPVYGGCGGNGNPFESREACBACFPV 412

Db 310 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEDDYCMAYC 360

RESULT 7

PCT-US04-42360-1362

Sequence 1362, Application PCT/TUS0442360

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation doing business as Massachusetts General

APPLICANT: Hospital / Bayer AG

TITLE OF INVENTION: Nucleotide sequences involved in pain

FILE REFERENCE: 17633/2048

CURRENT APPLICATION NUMBER: PCT/US04/42360

CURRENT FILING DATE: 2004-12-17

PRIOR APPLICATION NUMBER: 60/531,341

PRIOR FILING DATE: 19-Dec-2003

NUMBER OF SEQ ID NOS: 2587

SOFTWARE: Perl script

SEQ ID NO 1362

LENGTH: 763

TYPE: PRT

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Refseq / NP_057244

DATABASE ENTRY DATE: 2003-10-04

PCT-US04-42360-1362

Query Match

47.1% Score 155; DB 1; Length 763;

Best Local Similarity 54.9%; Pred. No. 3.1e-12;

Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNNKFKYSEKREYEC 53

Db 310 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEDDYCMAYC 360

RESULT 8

PCT-US04-42360-1136

Sequence 1136, Application PCT/TUS0442360

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation doing business as Massachusetts General

APPLICANT: Hospital / Bayer AG

TITLE OF INVENTION: Nucleotide sequences involved in pain

FILE REFERENCE: 17633/2048

CURRENT APPLICATION NUMBER: PCT/US04/42360

CURRENT FILING DATE: 2004-12-17

PRIOR APPLICATION NUMBER: 60/531,341

PRIOR FILING DATE: 19-Dec-2003

NUMBER OF SEQ ID NOS: 2587

SOFTWARE: Perl script

SEQ ID NO 1136

LENGTH: 765

TYPE: PRT

ORGANISM: Rattus norvegicus

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: SWISS-Prot / M1322

DATABASE ENTRY DATE: 2003-02-28

PCT-US04-42360-1136

Query Match

47.1% Score 155; DB 1; Length 765;

Best Local Similarity 54.9%; Pred. No. 3.1e-12;

Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNNKFKYSEKREYEC 53

Db 312 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEDDYCMAYC 362

RESULT 9

PCT-US04-42360-1360

Sequence 1360, Application PCT/TUS0442360

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation doing business as Massachusetts General

APPLICANT: Hospital / Bayer AG

; TITLE OF INVENTION: Nucleotide sequences involved in pain

; FILE REFERENCE: 17633/2048

; CURRENT APPLICATION NUMBER: PCT/US04/42360

; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: 60/531,341

; PRIOR FILING DATE: 19-Dec-2003

; NUMBER OF SEQ ID NOS: 2587

; SOFTWARE: Perl script

; SEQ ID NO 1360

; LENGTH: 765

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SWISS-Prot / M1322

; DATABASE ENTRY DATE: 2003-02-28

PCT-US04-42360-1360

Query Match

47.1% Score 155; DB 1; Length 765;

Best Local Similarity 54.9%; Pred. No. 3.1e-12;

Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNNKFKYSEKREYEC 53

Db 312 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEDDYCMAYC 362

RESULT 10

US-11-028-058-9

Sequence 9, Application US/11028058

GENERAL INFORMATION:

APPLICANT: HILL, JENNIFER J.

APPLICANT: MOLEMAN, NEIL M.

TITLE OF INVENTION: POLYSTATIN DOMAIN CONTAINING PROTEINS

FILE REFERENCE: 08702.0015-00

CURRENT APPLICATION NUMBER: US/11/028,058

CURRENT FILING DATE: 2005-01-04

PRIOR APPLICATION NUMBER: US/10/369,736

PRIOR FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: 60/357,846

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 60/434,645

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGTH: 552

TYPE: PRT

ORGANISM: Mus sp.

US-11-028-058-9

Query Match

45.6% Score 150; DB 7; Length 552;

Best Local Similarity 42.9%; Pred. No. 9.8e-12;

Matches 24; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 1 EACNLPYVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNNKFKYSEKREYEC 56

Db 361 DVICALPVGCPGCGMERPMAYSPILQCHPFTVYSGCBGNSNFTFRESCEBACPVF 416

RESULT 11

US-60-647-493-4

Sequence 4, Application US/60647493

GENERAL INFORMATION:

APPLICANT: Rubinstein, Amy

TITLE OF INVENTION: TRANSGENIC ZEBRAFISH MODELS FOR

FILE REFERENCE: 26007.0004U1

CURRENT APPLICATION NUMBER: US/60/647,493

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 547

Qy 1 EACNLPIRVGPCIAFFPRMAFPAVKGKCVLPFYGGCGGNGKIFYSEKECEHYCG 54
| : | | | | | | | | | | : | | |
Db 289 EVCSEQAEWGPCRAMISRWFVDVTEGKCAFFYGGCGGNNRNPDTIEYCAVAVCG 342

Search completed: February 23, 2005, 03:35:44
Job time : 40 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:30:15 ; Search time 2610 Seconds
(without alignments)
875.897 Million cell updates/sec

Title: US-10-038-722-27
Perfect score: 329
Sequence: 1 EACNLPIYRGCIAPPRMA.....QGNKFKYSEKREYGVVP 56

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 45554873 segs, 20411521753 residues
Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEVX1h
-Q=/cgn2_1/USPTO_epool/US10038722/runat_18022005_145204_14124/app_query.fasta.1.199
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=trpm -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORML=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10038722@cgn2_1.1.4972@runat_18022005_145204_14124 -NCPUB=6 -ICPU=3
-NO_MMAP -LARGESQUEERY -NEG SCORES=0 -WAIT -DSEPHLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*

- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
- 44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
- 61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
- 62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
- 63: /cgn2_6/ptodata/1/pna/US108A_COMB.seq:*
- 64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq:*
- 65: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
- 66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
- 67: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
- 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
- 70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
- 71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
- 72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
- 73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
- 74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
- 75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
- 76: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
- 77: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
- 78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
- 79: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
- 80: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
- 81: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
- 82: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
- 83: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
- 84: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
- 85: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
- 86: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
- 87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
- 88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
- 89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
- 90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
- 91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
- 92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq:*
- 93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq:*
- 94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
- 95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
- 96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
- 97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
- 98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
- 99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
- 100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
- 101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*


```

; SEQ ID NO 56
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: DNA sequence of the N-Terminal BglII-BamHI DX-890
US-10-361-997-56

Alignment Scores:
Pred. No.: 5.63e-34 Length: 195
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-56 (1-195)

Oy 1 GUAUACySaAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
Db 19 GAGGCTTGAATCTTCCCAATGTTAGAGCTCCATGATTTCTTTCCCAAGATGGCT 78

Oy 21 PheAspAlaValIyGlyLysCySValIeuPheProTyrgIyGlyCySgInGlyAsnGly 40
Db 79 TTCATGCTGTTAAGGTAAGTGTGTTTCCCATATGGTGGTTGCAAGTAACGGT 138

Oy 41 AsnIySPhetYrSerGIuLySgIuCyAArgGluTyrcySgIyValPro 56
Db 139 AACAAATTCTACTCTGAAGAAGATGTAGAGAACTGTGTGTTCCA 186

RESULT 3
US-10-361-997-72
; Sequence 72, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: DNA to insert at BspEI/KpnI site for 2nd encoding
US-10-361-997-72

Alignment Scores:
Pred. No.: 6.05e-34 Length: 207
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-72 (1-207)

Oy 1 GUUAUACySaAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
Db 28 GAGGCTTGAATCTTCCCAATGTTAGAGCTCCATGATTTCTTTCCCAAGATGGCT 87

Oy 21 PheAspAlaValIyGlyLysCySValIeuPheProTyrgIyGlyCySgInGlyAsnGly 40
Db 88 TTTCAGCGCTTAAAGGCAATGCGTCTTTTCTTCCATAGCGGCTTGCCAGGCAATGAC 147

Oy 41 AsnIySPhetYrSerGIuLySgIuCyAArgGluTyrcySgIyValPro 56
```

```

Db 148 AATAAATTTATGCGAGAAAGATGCGGTAGATTTGCGGCTCCCT 195

RESULT 4
US-08-849-406-73
; Sequence 73, Application US/08849406
; APPLICANT: Ley, Arthur C.
; LADNER, Robert C.
; GUTERMAN, Sonia K.
; ROBERTS, Bruce L.
; MARKLAND, William
; KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCE ADS: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,406
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16349
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-08-849-406-73

Alignment Scores:
Pred. No.: 1.53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-08-849-406-73 (1-444)

Oy 1 GUUAUACySaAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
Db 265 GAGGCTTGAATCTTCCCAATGTTAGAGCTCCATGATTTCTTTCCCAAGATGGCT 324

Oy 21 PheAspAlaValIyGlyLysCySValIeuPheProTyrgIyGlyCySgInGlyAsnGly 40
Db 325 TTCACGCTGTTAAGGTAAGTGTGTTTCCCATATGGTGGTTGCAAGTAACGGT 384

Oy 41 AsnIySPhetYrSerGIuLySgIuCyAArgGluTyrcySgIyValPro 56
Db 385 AACAAATTCTACTCTGAAGAAGATGTAGAGAACTGTGTGTTCCA 432
```


RESULT 5
US-08-849-406A-73
Sequence 73, Application US/08849406A
APPLICANT: LEY, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-08-849-406A-73
Alignment Scores:
Pred. No.: 1,53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-038-722-27 (1-56) x US-08-849-406A-73 (1-444)
QY 1 GIUAlaCyAsAnLeuProIleValaRgLyProCySIlleAlaPhePheProArGTTPaLa 20
DB 265 GAGGCTTGAAGTTCGCAATCGCAGAGGTGCATGCAATGCTTTCTTCCCAAGATGGGCT 324
QY 21 PheAsPaLaValIySgLyCySValIleuPheProTyRgLyCySgInglyAengLy 40
DB 325 TTCGACGCTGTTAAGGTAAAGGTAGCGCTTCTTCCCATACGGTGGTTGTCAAGGTAAACGGT 384
QY 41 AenLySPhetYrSerGluYsGluCySArGluTyRyCySgLyValPro 56
DB 385 AACAGTTCTACTCTGAGAAGAGGTGTACAGAGTACTGTGTGTCCA 432
RESULT 6
US-10-038-722-73
Sequence 73, Application US/10038722

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patent In version 3.1
SEQ ID NO 73
LENGTH: 444
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BactB-EcORI cassette for expression of Epi-HNE-4 (Table 252
US-10-038-722-73
Alignment Scores:
Pred. No.: 1,53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 46 Gaps: 0
US-10-038-722-27 (1-56) x US-10-038-722-73 (1-444)
QY 1 GIUAlaCyAsAnLeuProIleValaRgLyProCySIlleAlaPhePheProArGTTPaLa 20
DB 265 GAGGCTTGAAGTTCGCAATCGCAGAGGTGCATGCAATGCTTTCTTCCCAAGATGGGCT 324
QY 21 PheAsPaLaValIySgLyCySValIleuPheProTyRgLyCySgInglyAengLy 40
DB 325 TTCGACGCTGTTAAGGTAAAGGTAGCGCTTCTTCCCATACGGTGGTTGTCAAGGTAAACGGT 384
QY 41 AenLySPhetYrSerGluYsGluCySArGluTyRyCySgLyValPro 56
DB 385 AACAGTTCTACTCTGAGAAGAGGTGTACAGAGTACTGTGTGTCCA 432
RESULT 7
US-10-361-997-58
Sequence 58, Application US/10361997
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 1965
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal
OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion coding region
US-10-361-997-58

Alignment Scores:

Pred. No.: 9.41e-33 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-58 (1-1965)

QY 1 GIUAlaCYsaenLeuProIleValaIrgGlyProCYsIleAlaPhePheProArgrTrpAla 20
DB 1 GAAGCCTGTAACCTTCCCAATGTGTAGAGGTCATGTATGCTTCTCCCAAGATGGGCT 60
QY 21 PheAspAlaValIyGlyGlyCyseValIleuPheProTYrGlyGlyCYseGlnGlyAsnGly 40
DB 61 TTCGATGCTGTTAAGGTAAGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAACGCT 120
QY 41 AsnIySPheTYrSerGIuLyGlyCyseArgrGIuTYrCYseGlyValPro 56
DB 121 AACAGTCTACTCTGAAGAAAGATGTAGAGAAATCTGTGCTTCCA 168

RESULT 8

US-10-361-997-60

; Sequence 60, Application US/10361997

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.

; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES

; FILE REFERENCE: 3421.1015-000

; CURRENT APPLICATION NUMBER: US/10/361,997

; PRIOR FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 60/355,547

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 60

; LENGTH: 1965

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: DNA sequence of the C-terminal

; OTHER INFORMATION: albumin-(GGS)4GG-DX-890 fusion coding region

US-10-361-997-60

Alignment Scores:

Pred. No.: 9.41e-33 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-60 (1-1965)

QY 1 GIUAlaCYsaenLeuProIleValaIrgGlyProCYsIleAlaPhePheProArgrTrpAla 20
DB 1798 GAAGCCTGTAACCTTCCCAATGTGTAGAGGTCATGTATGCTTCTCCCAAGATGGGCT 1857
QY 21 PheAspAlaValIyGlyGlyCyseValIleuPheProTYrGlyGlyCYseGlnGlyAsnGly 40
DB 1858 TTCGATGCTGTTAAGGTAAGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAACGCT 1917
QY 41 AsnIySPheTYrSerGIuLyGlyCyseArgrGIuTYrCYseGlyValPro 56
DB 1918 AACAGTCTACTCTGAAGAAAGATGTAGAGAAATCTGTGCTTCCA 1965

RESULT 9

US-10-361-997-70

; Sequence 70, Application US/10361997

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.

; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES

; FILE REFERENCE: 3421.1015-000

; CURRENT APPLICATION NUMBER: US/10/361,997

; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 60/355,547

; PRIOR FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 70

; LENGTH: 3255

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: NotI cassette of pDB2300X2 with DX890 (Nterm) and

; OTHER INFORMATION: Cterm linker ready for second DX890

US-10-361-997-70

Alignment Scores:

Pred. No.: 1.74e-32 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-70 (1-3255)

QY 1 GIUAlaCYsaenLeuProIleValaIrgGlyProCYsIleAlaPhePheProArgrTrpAla 20
DB 901 GAAGCCTGTAACCTTCCCAATGTGTAGAGGTCATGTATGCTTCTCCCAAGATGGGCT 960
QY 21 PheAspAlaValIyGlyGlyCyseValIleuPheProTYrGlyGlyCYseGlnGlyAsnGly 40
DB 961 TTCGATGCTGTTAAGGTAAGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAACGCT 1020
QY 41 AsnIySPheTYrSerGIuLyGlyCyseArgrGIuTYrCYseGlyValPro 56
DB 1021 AACAGTCTACTCTGAAGAAAGATGTAGAGAAATCTGTGCTTCCA 1068

RESULT 10

US-10-361-997-73

; Sequence 73, Application US/10361997

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.

; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES

; FILE REFERENCE: 3421.1015-000

; CURRENT APPLICATION NUMBER: US/10/361,997

; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 60/355,547

; PRIOR FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 73

; LENGTH: 3440

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: DNA sequence of NotI cassette of pDB2300X3 with 2

; OTHER INFORMATION: x DX-890

US-10-361-997-73

Alignment Scores:

Pred. No.: 1.86e-32 Length: 3440
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-73 (1-3440)

QY 1 GIUAlaCYsaenLeuProIleValaIrgGlyProCYsIleAlaPhePheProArgrTrpAla 20

Db 901 GAAGCTGTAAGCTTGGCAATGTTAGAGTTCATGATGATTCCTTCCCAAGATGGCT 960
Qy 21 PheAaPAlaValIySgIyScyValIleuPheProTyrgIyGlyCySgInglYaaNgly 40
Db 961 TTTCGATGCTGTAAGGTAAGTGTGTTTGTTCCTATGAGTGAGTGAAGTAACGCT 1020
Qy 41 AaenLySphetYSerGluTySgIyCySaAArgIuTyrcYsGlyValPro 56
Db 1021 AACCAATCTACTCTGAAAGAGATGACGAATACTGTGTGTTCCA 1068
RESULT 11
US-10-361-997-44
Sequence 44, Application US/10361997
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 3444
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DPI-14- (GGS) 4 GG-rHA- (GGS) 4-GG-DX-890 DNA sequence
US-10-361-997-44
Alignment Scores:
Pred. No.: 1,87e-32 Length: 3444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0
US-10-038-722-27 (1-56) x US-10-361-997-44 (1-3444)
Qy 1 GluaIaCyAaenLeuProIleValaIArgIyProCySalleaIaPheProAArgITrAlaPhe 20
Db 2920 GAGGCTTGAATCTTCTATCGTCCTGGCCCTTGATGATGCTTTTCTCGTTGGGCC 2979
Qy 21 PheAaPAlaValIySgIyScyValIleuPheProTyrgIyGlyCySgInglYaaNgly 40
Db 2980 TTTCGATGCTGTAAGGTAAGTGTGTTTGTTCCTATGAGTGAGTGAAGTAACGCT 3039
Qy 41 AaenLySphetYSerGluTySgIyCySaAArgIuTyrcYsGlyValPro 56
Db 3040 AATTAATTTATAGCGAAGAGTCCGTAAGTATGCGGCGCTCCT 3087
RESULT 12
US-08-849-406-71
Sequence 71, Application US/08849406
APPLICANT: Ley, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA

ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 8584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-08-849-406-71
Alignment Scores:
Pred. No.: 2.65e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0
US-10-038-722-27 (1-56) x US-08-849-406-71 (1-8584)
Qy 2 AlaCyAaenLeuProIleValaIArgIyProCySalleaIaPheProAArgITrAlaPhe 21
Db 1212 GCTGTACTGATGCGCAATGTCAGAGTCAATGCTTCTTCCCAAGATGGGCTTTC 1271
Qy 22 AaPAlaValIySgIyScyValIleuPheProTyrgIyGlyCySgInglYaaNglyAaen 41
Db 1272 GAGGCTGTAAGGTAAGTGTGTTTGTTCCTATGAGTGAGTGAAGTAACGCTAAC 1331
Qy 42 LysPheTySerGluTySgIyCySaAArgIuTyrcYsGlyValPro 56
Db 1332 AAGTCTACTCTGAGAGAGATGTAAGATGACTGTGTGTTCCA 1376
RESULT 13
US-08-849-406A-71
Sequence 71, Application US/08849406A
APPLICANT: Ley, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 8584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-08-849-406A-71

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-08-849-406A-71 (1-8584)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 1212 GCTGTACTCTCCCAATGCTCAGAGTCCATGCTTTCTTCCCAAGATGGCTTTC 1271
QY 22 AspaIaValLySgLyVysCyValIleuPheProTyrgLygLyCySgInGlyAaNgLyAa 41
DB 1272 GACGCTGTTAAGGTAAGTGGCTCTTGTCCCATACGGGTGTGCAAGGTAAACGTTAC 1331
QY 42 LysPheTySerGluLyGluCyAaArgGluTyrcySgLyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 1376

RESULT 14
US-10-038-722-71
Sequence 71, Application US/10038722
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO 71
LENGTH: 8584

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pHL-D2 (pFalphaPrepro::BPI-HNE-3) (Table 251)
US-10-038-722-71

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-10-038-722-71 (1-8584)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 1212 GCTGTACTCTCCCAATGCTCAGAGTCCATGCTTTCTTCCCAAGATGGCTTTC 1271
QY 22 AspaIaValLySgLyVysCyValIleuPheProTyrgLygLyCySgInGlyAaNgLyAa 41
DB 1272 GACGCTGTTAAGGTAAGTGGCTCTTGTCCCATACGGGTGTGCAAGGTAAACGTTAC 1331
QY 42 LysPheTySerGluLyGluCyAaArgGluTyrcySgLyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGTGTCCA 1376

RESULT 15
US-08-849-406-75
Sequence 75, Application US/08849406
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8590 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 75;
US-08-849-406-75

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-08-849-406-75 (1-8590)

QY	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe	21
DB	1212	GCTGTAACTTCCCAATCCTCAGAGGTCATGCAATTCCTTCTCCCAAGATGGGCTTTC	1271
QY	22	AspAlaValLysGlyLysCysValLeuPheProTyrGlyCysGlnGlyAsnGlyAsn	41
DB	1272	GACGCTTAAGGTAAGTACGCTGCTGTTCCCATACGGTGTGTCAAGTAAAGGTAAAC	1331
QY	42	LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
DB	1332	AAGTCTACTCTGAGAGAGAGGTAGAGACTGTGTGTTCCA	1376

Search completed: February 23, 2005, 04:19:26
Job time : 2615 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:30:45 ; Search time 591 Seconds

(without alignments)
61.077 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIVRGPCIAFPFRMA.....QGNGKFKYSEKREYCVGP 56

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5167335 seqs, 322287606 residues

Total number of hits satisfying chosen parameters: 10334670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cg2_1/USPFO.spool/US10038722/runat_18022005_145204_14132/app_query.fasta.1.199
-DB=Pending Patents NA_New -QPM=fastap -SUFFIX=tmpn -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10038722_QCGN_1.1_223@runat_18022005_145204_14132 -NCPU=6 -ICPU=3
-NO_MAP -LARGEOBJECT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_New:*

1:	/cg2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2:	/cg2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3:	/cg2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4:	/cg2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5:	/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6:	/cg2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7:	/cg2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
8:	/cg2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
9:	/cg2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	90.0	1436	7	US-10-485-231-7
2	182	55.3	1731	8	US-11-028-058-6
3	182	55.3	1923	8	US-11-028-058-4
4	176	53.5	1716	8	US-11-028-058-1
5	176	53.5	1716	8	US-11-028-058-2
6	176	53.5	1716	8	US-11-028-058-48
7	176	52.3	1695	8	US-11-028-058-10
8	155	47.1	3727	1	PCT-US04-42360-1137
9	155	47.1	3727	1	PCT-US04-42360-1361

10	150	45.6	1659	8	US-11-028-058-8
11	146	44.4	669	7	US-10-287-436A-1006
12	146	44.4	3414	6	US-10-450-763-19078
13	146	44.4	3579	6	US-10-287-436A-118
14	146	44.4	3585	7	US-10-450-763-19077
15	144	43.8	1409	6	US-10-495-300-27
16	144	43.8	1544	8	US-11-050-926-301
17	144	43.8	1558	8	US-11-050-926-103
18	141.5	43.0	3238	7	US-10-450-763-19079
19	135	41.0	180	5	US-09-700-179B-3
20	135	41.0	180	5	US-09-700-179B-50
21	135	41.0	252	5	US-09-700-179B-17
22	135	41.0	252	5	US-09-700-179B-58
23	134	40.7	4069	7	US-10-450-763-19946
24	133	40.4	180	5	US-09-700-179B-15
25	133	40.4	252	5	US-09-700-179B-15
26	133	40.4	252	5	US-09-700-179B-56
27	133	40.4	10558	6	US-10-852-335A-66
28	133	40.4	10558	6	US-10-287-436A-151
29	133	40.4	10558	6	US-10-287-436A-764
30	129	39.2	1142	8	US-11-050-926-315
31	127	38.6	941	7	US-10-485-231-25
32	123	37.4	408	5	US-09-700-179B-43
33	123	37.4	408	5	US-09-700-179B-54
34	122	37.1	180	5	US-09-700-179B-5
35	122	37.1	252	5	US-09-700-179B-52
36	122	37.1	252	5	US-09-700-179B-19
37	122	37.1	252	5	US-09-700-179B-60
38	115	35.0	148	8	PCT-US05-02350-349
39	115	35.0	148	8	US-11-043-770-349
40	115	35.0	1252	1	PCT-US05-02350-342
41	115	35.0	1252	8	US-11-043-770-342
42	115	35.0	1294	5	US-09-999-570A-47
43	115	35.0	1307	5	US-09-999-570A-95
44	115	35.0	1309	1	PCT-US05-02350-343
45	115	35.0	1309	8	US-11-043-770-343

ALIGNMENTS

RESULT 1
US-10-485-231-7
; Sequence 7, Application US/10485231
; GENERAL INFORMATION:
; APPLICANT: GENSET
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 142.WO1
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 60/311,305
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/314,734
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/318,204
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/326,470
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..263
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 264..926
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 927..1436
; FEATURE:

NAME/KEY: polyA signal
 LOCATION: 1404..1409
 FEATURE:
 NAME/KEY: polyA site
 LOCATION: 1421..1436
 US-10-485-231-7

Alignment Scores:
 Pred. No.: 2,33e-29 Length: 1436
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 7 Gaps: 0

US-10-038-722-27 (1-56) x US-10-485-231-7 (1-1436)

QY 2 AAlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTTPAlaPhe 21
 DB 1117 GCCTCAATCTCCCATATGTCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATTT 1176
 QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 1177 GATGCTGTCAGAGGAGGAGGCGCTCTCCCTACGCGGCGCTGCCAGGCAACGGGAAAC 1236
 QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
 DB 1237 AAGTTTACTCAGAGAGAGAGTGCAGAGTACTGCGGTGCTCT 1281

RESULT 2
 US-11-028-058-6
 Sequence 6, Application US/11028058

GENERAL INFORMATION:
 APPLICANT: HILL, JENNIFER J.
 APPLICANT: WOLFMAN, NEIL M.
 TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 FILE REFERENCE: 08702.0015-00
 CURRENT APPLICATION NUMBER: US/11/028,058
 PRIOR FILING DATE: 2005-01-04
 PRIOR APPLICATION NUMBER: US/10/369,736
 PRIOR FILING DATE: 2003-02-21
 PRIOR APPLICATION NUMBER: 60/357,846
 PRIOR FILING DATE: 2002-02-21
 PRIOR APPLICATION NUMBER: 60/434,645
 PRIOR FILING DATE: 2002-12-20
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 1731
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-028-058-6

Alignment Scores:

Pred. No.: 4.47e-14 Length: 1731
 Score: 182.00 Matches: 29
 Percent Similarity: 70.91% Conservative: 10
 Best Local Similarity: 52.73% Mismatches: 16
 Query Match: 55.32% Indels: 0
 DB: 8 Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-6 (1-1731)

QY 2 AAlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTTPAlaPhe 21
 DB 1153 GCGTGCAGCTCCCGCCCTGCAGGGGCGCTCCAAAGCCTTCGCTGCGGCTTAC 1212
 QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 1213 AACAGCAACAGGGGCGGAGTGCAGTCTTGTCTATGTGTGCTGCGAGGCAATGGCAAC 1272
 QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

DB 1273 AACTTGAGAGCCGTGAGGCGCTGTGAGAGTGTGCCCCCTTCCCC 1317

RESULT 3
 US-11-028-058-4

GENERAL INFORMATION:
 APPLICANT: HILL, JENNIFER J.
 APPLICANT: WOLFMAN, NEIL M.
 TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 FILE REFERENCE: 08702.0015-00
 CURRENT APPLICATION NUMBER: US/11/028,058
 PRIOR FILING DATE: 2005-01-04
 PRIOR APPLICATION NUMBER: US/10/369,736
 PRIOR FILING DATE: 2003-02-21
 PRIOR APPLICATION NUMBER: 60/357,846
 PRIOR FILING DATE: 2002-02-21
 PRIOR APPLICATION NUMBER: 60/434,645
 PRIOR FILING DATE: 2002-12-20
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 1923
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (732)
 OTHER INFORMATION: a, t, c or g
 US-11-028-058-4

Alignment Scores:

Pred. No.: 5.07e-14 Length: 1923
 Score: 182.00 Matches: 29
 Percent Similarity: 70.91% Conservative: 10
 Best Local Similarity: 52.73% Mismatches: 16
 Query Match: 55.32% Indels: 0
 DB: 8 Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-4 (1-1923)

QY 2 AAlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTTPAlaPhe 21
 DB 1345 GCGTGCAGCTCCCGCCCTGCAGGGGCGCTCCAAAGCCTTCGCTGCGGCTTAC 1404
 QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 1405 AACAGCAACAGGGGCGGAGTGCAGTCTTGTCTATGTGTGCTGCGAGGCAATGGCAAC 1464
 QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
 DB 1465 AACTTGAGAGCCGTGAGGCGCTGTGAGAGTGTGCCCCCTTCCCC 1509

RESULT 4
 US-11-028-058-1

GENERAL INFORMATION:
 APPLICANT: HILL, JENNIFER J.
 APPLICANT: WOLFMAN, NEIL M.
 TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 FILE REFERENCE: 08702.0015-00
 CURRENT APPLICATION NUMBER: US/11/028,058
 PRIOR FILING DATE: 2005-01-04
 PRIOR APPLICATION NUMBER: US/10/369,736
 PRIOR FILING DATE: 2003-02-21
 PRIOR APPLICATION NUMBER: 60/357,846
 PRIOR FILING DATE: 2002-02-21
 PRIOR APPLICATION NUMBER: 60/434,645
 PRIOR FILING DATE: 2002-12-20
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1716
 TYPE: DNA

```
; ORGANISM: Mus sp.  
US-11-028-058-1  
  
Alignment Scores:  
Pred. No.:      2.78e-13          Length:       1716  
Score:           176.00            Matches:        28  
Percent Similarity:    68.52%     Conservative:   9  
Best Local Similarity:    51.85%     Mismatches:   17  
Query Match:             53.50%     Indels:         0  
DB:                       8              Gaps:         0  
  
US-10-038-722-27 (1-56) x US-11-028-058-1 (1-1716)  
  
QY               3 CysAsnLeuPrcIleValAlArgGlyProCysIleAlaphepheProArGTTPAlApeasp 22  
Dd              1141 TGCAGCCCTGCCCTCGCCCTCAAGGGCTTGCAAAGCTTATGTCCCACGCTGGGCTTAACAAC 1200  
                  ::::::::::::::::::::|:::|||||||  
OY                23 AlaValLySGILyLycCyseValLeupeProTYrGIyGLICySgInGLyASngLYASnGLyASNLYS 42  
Db              1201 AGCCAAGAAGGCTTATGCCAGTCCTTCCTATTAGCGGCGGTGTGAAGGCAAGGTAACAAC 1260  
                  ::::|||||  
OY                43 PheTySerGIuLySLuCyeARgiLuTyryCYsgIValpro 56  
Dd              1261 TTtGAAGcCcgtGaAgcTTGTtgAGAGAtgcTctccTTcccG 1302  
                  |||||::|  
  
RESULT 5  
US-11-028-058-2  
; Sequence 2, Application US/11028058  
; GENERAL INFORMATION:  
APPLICANT: HILL, JENNIFER J.  
APPLICANT: WOLFMAN, NEIL M.  
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS  
FILE REFERENCE: 08702.0015-00  
CURRENT APPLICATION NUMBER: US/11/028,058  
PRIOR FILING DATE: 2005-01-04  
PRIOR APPLICATION NUMBER: US/10/369,736  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 60/357,846  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/434,645  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1716  
TYPE: DNA  
ORGANISM: Mus sp.  
US-11-028-058-2  
  
Alignment Scores:  
Pred. No.:      2.78e-13          Length:       1716  
Score:           176.00            Matches:        28  
Percent Similarity:    68.52%     Conservative:   9  
Best Local Similarity:    51.85%     Mismatches:   17  
Query Match:             53.50%     Indels:         0  
DB:                       8              Gaps:         0  
  
US-10-038-722-27 (1-56) x US-11-028-058-2 (1-1716)
```

```

; Sequence 48 Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1713)
US-11-028-058-48

Alignment Scores:
Pred. No.: 2.78e-13 Length: 1716
Score: 176.00 Matches: 28
Percent Similarity: 68.52% Conservative: 9
Best Local Similarity: 51.85% Mismatches: 17
Query Match: 53.50% Indels: 0
Db: 8 Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-48 (1-1716)

QY 3 CysasnupeuprollevalarxglyProcyatlealaphenheProaxgtrpalapheap 22
Db 1141 TGCAGCCCTGCTGCCCTGCAGAGGCGCTTGCAAGCTTATGTCACCGCTGGCTTACAC 12000
QY 23 Alavalysglylyscysvalleupeheprotyrlyglycysglinglyasnglyasnllys 42
Db 1201 AGCCAGACAGGCCCTATGCACTCCTCTCTATGCGGCTGTGAGGCGAAGCTAACAC 1266
QY 43 PheTySerGluysGluCySarxglyuTyrcysglyvalPro 56
Db 1261 TTTGAAGCGCTGAGGCTTGAGAGGAGTGTGCTCCCTCCG 1302

RESULT 7
US-11-028-058-10
; Sequence 10, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-058-10

Alignment Scores:
Pred. No.: 9.35e-13 Length: 1695

```



```

CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: 60/531,341
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: perl script
SEQ ID NO 1361
LENGTH: 3727
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NM_016160
DATABASE ENTRY DATE: 2003-10-04
PCT-US04-42360-1361

Alignment Scores:
Pred. No.: 4.44e-10 Length: 3727
Score: 155.00 Matches: 28
Percent Similarity: 58.82% Conservative: 2
Best Local Similarity: 54.90% Mismatches: 21
Query Match: 47.11% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x PCT-US04-42360-1361 (1-3727)

Oy 3 CysAsnLeuProIleValArgGlyProCysIleAlaPhePheProAsgTrpAlaPheAsp 22
Db 1000 TGTCTCCAGAGAGCGAATGACGGGGCCCTGCGGGCCGTATGCTCGTGTACTTGAC 1059
Oy 23 AlaValIysGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsnLys 42
Db 1060 CTCCTCCAGGAAGTACGTCGCTTATATATGTGTGGCTGCGGCGCAACAGAACAT 1159
Oy 43 PheTyrSerGlnLysGlnCysArgGlyTyrCys 53
Db 1120 TTTGAGTCTGAGATATTGATGCGCTGTGTGT 1152

RESULT 10
US-11-028-058-8
; Sequence 8, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: MOLEMAN, NEIL M.
; TITLE OR INVENTION: POLYSTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-028-058-8

Alignment Scores:
Pred. No.: 7.76e-10 Length: 1659
Score: 150.00 Matches: 24
Percent Similarity: 60.71% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 22
Query Match: 45.59% Indels: 0
DB: 8 Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-8 (1-1659)

Oy 1 GluAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProAsgTrpAla 20
Db 1000 TGTCTCCAGAGAGCGAATGACGGGGCCCTGCGGGCCGTATGCTCGTGTACTTGAC 1059

```

```
Db 1081 GATGTCTGTGACCTGCTGACGAGGGCCCTGCGAGGCTGGAGCCACGCTGGGCC 1140
Qy 21 PheaspaIaValIySgIyCyseValIeupheProTyrgIyCyseGInglYAsnGly 40
Db 1141 TACAGCCACCTGCTACACAGGAGCCACCCCTTTGATACAGTGCGCTGAGAGAAACAGC 1200
Qy 41 AsnIySphETyrsErgIuIySgIuCyseArGluTyrgIyCyseGlyValPro 56
Db 1201 AATACCTTTGACACCGGAGAGCTGTGAGATGCTTCCCTGTACCA 1248

RESULT 11
US-10-287-436A-1006
; Sequence 1006, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1006
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-1006

Alignment Scores:
Pred. No.: 8.88e-10 Length: 669
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
Gaps: 0
DB: 6

US-10-038-722-27 (1-56) x US-10-287-436A-1006 (1-669)

Qy 1 GluIaCyseAsnLeuProIleValaIrgIyProCyseIleAlaPhePheProArGTrpAla 20
Db 184 GAGGTGCTCTGACACAGCCGAGAGCGGGCCGTGCCAGCAATGATCTCCGCTGTAC 243
Qy 21 PheaspaIaValIySgIyCyseValIeupheProTyrgIyCyseGInglYAsnGly 40
Db 244 TTTGATGTGACTGAGAGGAGAGTGCCCCATTCTTTACGGCGGATGTGGCGGCAACCGG 303
Qy 41 AsnIySphETyrsErgIuIySgIuCyseArGluTyrgIyCyseGly 54
Db 304 AACCACTTTGACACAGAGAGTACTGATGCGCGGTGTGGC 345

RESULT 12
US-10-450-763-19078
; Sequence 19078, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 19078
; LENGTH: 3414
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1075) ..(1683)
; OTHER INFORMATION: 99% homologous to Homo sapiens APP precursor, accession number
; OTHER INFORMATION: AJ1584, Smith-Waterman Score=1130.
US-10-450-763-19078

Alignment Scores:
Pred. No.: 6.31e-09 Length: 3414
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
DB: 7

US-10-038-722-27 (1-56) x US-10-450-763-19078 (1-3414)

Qy 1 GluIaCyseAsnLeuProIleValaIrgIyProCyseIleAlaPhePheProArGTrpAla 20
Db 2266 GAGGTGCTCTGACACAGCCGAGAGCGGGCCGTGCCAGCAATGATCTCCGCTGTAC 2325
Qy 21 PheaspaIaValIySgIyCyseValIeupheProTyrgIyCyseGInglYAsnGly 40
Db 2326 TTTGATGTGACTGAGAGGAGAGTGCCCCATTCTTTACGGCGGATGTGGCGGCAACCGG 2385
Qy 41 AsnIySphETyrsErgIuIySgIuCyseArGluTyrgIyCyseGly 54
Db 2386 AACCACTTTGACACAGAGAGTACTGATGCGCGGTGTGGC 2427

RESULT 13
US-10-287-436A-118
; Sequence 118, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-118

Alignment Scores:
Pred. No.: 6.68e-09 Length: 3579
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
DB: 6

US-10-038-722-27 (1-56) x US-10-287-436A-118 (1-3579)

Qy 1 GluIaCyseAsnLeuProIleValaIrgIyProCyseIleAlaPhePheProArGTrpAla 20
Db 1012 GAGGTGCTCTGACACAGCCGAGAGCGGGCCGTGCCAGCAATGATCTCCGCTGTAC 1071
Qy 21 PheaspaIaValIySgIyCyseValIeupheProTyrgIyCyseGInglYAsnGly 40
Db 1072 TTTGATGTGACTGAGAGGAGAGTGCCCCATTCTTTACGGCGGATGTGGCGGCAACCGG 1131
Qy 41 AsnIySphETyrsErgIuIySgIuCyseArGluTyrgIyCyseGly 54
Db 1132 AACCACTTTGACACAGAGAGTACTGATGCGCGGTGTGGC 1173

RESULT 14
US-10-450-763-19077
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 04:29:32 ; Search time 1772 Seconds

(without alignments)
186.788 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYRGCIAFFPRWA.....QGNNGKFKYSEKREYCVGP 56

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODL=frame_plus_p2n.model -DEV-xlh
-O=/cgcn2_1/USPFO/US10038722/runat_18022005_145236_14375/app_query_faeta_1.199
-DB=Published Applications NA -OFMT=faetap -SUFFIX=rmpb -MINMATCH=0.1
-LOOBL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10038722.0CGN_1.1.678.0runat_18022005_145236_14375
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONELOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.*

- 1: /cgcn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgcn2_6/ptodata/1/pubpna/PCF_NEW_PUB.seq.*
- 3: /cgcn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgcn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgcn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgcn2_6/ptodata/1/pubpna/PCFUS_PUBCOMB.seq.*
- 7: /cgcn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgcn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgcn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 10: /cgcn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgcn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgcn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgcn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgcn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgcn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgcn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgcn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgcn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgcn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgcn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgcn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgcn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	190	US-10-361-997-57	Sequence 57, Appl
2	329	100.0	195	US-10-361-997-56	Sequence 56, Appl
3	329	100.0	207	US-10-361-997-72	Sequence 72, Appl
4	329	100.0	444	US-10-038-722-73	Sequence 73, Appl
5	329	100.0	1965	US-10-361-997-58	Sequence 58, Appl
6	329	100.0	1965	US-10-361-997-60	Sequence 60, Appl
7	329	100.0	3255	US-10-361-997-70	Sequence 70, Appl
8	329	100.0	3444	US-10-361-997-73	Sequence 73, Appl
9	329	100.0	3444	US-10-361-997-74	Sequence 74, Appl
10	324	98.5	8584	US-10-038-722-71	Sequence 71, Appl
11	324	98.5	8590	US-10-038-722-75	Sequence 75, Appl
12	296	90.0	204	US-10-298-796-27	Sequence 27, Appl
13	296	90.0	408	US-09-918-995-8710	Sequence 8710, Ap
14	296	90.0	441	US-10-298-796-28	Sequence 28, Appl
15	296	90.0	1280	US-10-291-265-214	Sequence 214, Ap
16	296	90.0	1436	US-09-978-418-7	Sequence 7, Appl
17	296	90.0	1444	US-09-925-301-333	Sequence 333, Ap
18	296	90.0	1464	US-10-291-265-686	Sequence 666, Ap
19	296	90.0	1721	US-10-291-172-93	Sequence 93, Appl
20	296	90.0	1721	US-10-221-278-93	Sequence 28, Appl
21	296	90.0	1781	US-10-119-926-48	Sequence 7, Appl
22	281	85.4	512	US-09-918-995-30403	Sequence 30403, A
23	277	84.2	466	US-09-918-995-31769	Sequence 31769, A
24	269	81.8	435	US-09-960-352-4435	Sequence 4435, Ap
25	261	79.3	120239	US-10-352-281-271	Sequence 271, Ap
26	258	78.4	698	US-10-404-460-16	Sequence 16, Appl
27	230	69.9	393	US-09-960-352-5187	Sequence 5187, Ap
28	225	68.4	241	US-09-960-352-9174	Sequence 9174, Ap
29	205	62.3	353	US-09-960-352-15044	Sequence 15044, A
30	182	55.3	1731	US-10-369-738-6	Sequence 6, Appl
31	182	55.3	1923	US-10-369-738-4	Sequence 4, Appl
32	182	55.3	2948	US-10-007-280A-129	Sequence 129, App
33	182	55.3	3063	US-10-007-280A-130	Sequence 130, App
34	182	55.3	3301	US-09-794-589-1	Sequence 1, Appl
35	182	55.3	3301	US-10-315-380-1	Sequence 1, Appl
36	176	53.5	1716	US-10-369-738-1	Sequence 1, Appl
37	176	53.5	1716	US-10-369-738-2	Sequence 2, Appl
38	176	53.5	1716	US-10-369-738-48	Sequence 48, Appl
39	173	52.6	202	US-10-361-997-50	Sequence 50, Appl
40	173	52.6	207	US-10-361-997-49	Sequence 49, Appl
41	173	52.6	1977	US-10-361-997-51	Sequence 51, Appl
42	173	52.6	1977	US-10-361-997-53	Sequence 53, Appl
43	172	52.3	1476	US-10-021-963-1	Sequence 1, Appl
44	172	52.3	1476	US-10-029-386-24789	Sequence 24789, A
45	172	52.3	1647	US-10-239-663-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-361-997-57
Sequence 57, Application US/10361997
Publication No. US20040171794A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 190
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: DNA sequence of the C-Terminal BamHI-HindIII
OTHER INFORMATION: DX-890 cDNA
US-10-361-997-57

Alignment Scores:

Pred. No.:	6,72e-41	Length:	130
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-038-722-27 (1-56) x US-10-361-997-57 (1-190)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 13 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTTCTTCCCAAGATGGGCT 72
QY 21 PheAspAlaValIleGlyLysCySValLeuPheProTyrgIlyGlyCySgInglyAsngly 40
DB 73 TTCGATGCTTAAGGTAAAGTGTGTTTGTCCCATATGATGATGTTGTCAAGGTAAAGGT 132
QY 41 AsnIlePheTySerGluLysGluCyAsArgGluTyrcySgIlyValPro 56
DB 133 AACAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 180

RESULT 2

US-10-361-997-56
Sequence 56, Application US/10361997
Publication No. US2004017194A1

GENERAL INFORMATION:

APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 195
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal BglII-BamHI DX-890
OTHER INFORMATION: cDNA
US-10-361-997-56

Alignment Scores:

Pred. No.:	6,94e-41	Length:	195
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-038-722-27 (1-56) x US-10-361-997-56 (1-195)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTTCTTCCCAAGATGGGCT 78
QY 21 PheAspAlaValIleGlyLysCySValLeuPheProTyrgIlyGlyCySgInglyAsngly 40
DB 79 TTCGATGCTTAAGGTAAAGTGTGTTTGTCCCATATGATGATGTTGTCAAGGTAAAGGT 138
QY 41 AsnIlePheTySerGluLysGluCyAsArgGluTyrcySgIlyValPro 56
DB 139 AACAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 186

RESULT 3

US-10-361-997-72
Sequence 72, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:

APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 207
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA to insert at BspEI/KpnI site for 2nd encoding
US-10-361-997-72

Alignment Scores:

Pred. No.:	7,47e-41	Length:	207
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-038-722-27 (1-56) x US-10-361-997-72 (1-207)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 28 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTTCTTCCCAAGATGGGCT 87
QY 21 PheAspAlaValIleGlyLysCySValLeuPheProTyrgIlyGlyCySgInglyAsngly 40
DB 88 TTCGATGCTTAAGGTAAAGTGTGTTTGTCCCATATGATGATGTTGTCAAGGTAAAGGT 147
QY 41 AsnIlePheTySerGluLysGluCyAsArgGluTyrcySgIlyValPro 56
DB 148 AATAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 195

RESULT 4

US-10-038-722-73
Sequence 73, Application US/10038722
Publication No. US20030175919A1

GENERAL INFORMATION:

APPLICANT: Ley, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-18
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 444
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: BstE1-AatII-EcoRI cassette for expression of Epi-HNE-4 (Table 252)
OTHER INFORMATION:)
US-10-038-722-73

Alignment Scores:
Pred. No.: 1,938-40 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-038-722-27 (1-56) x US-10-038-722-73 (1-444)

QY 1 GIUAIACyAaenleuprollevalargylprocygsllealaphhepProargtrpala 20
DB 265 GAGGCTGTACTGCAATGCGAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 324

QY 21 PheapAlaVallylgllylscCyvalleupheProTyrGlylCygsInglyangly 40
DB 325 TTCGACGCTGTAAGGTAAAGTGCCTGTTCCCATAGGCTGTGTCAAGTAAAGGT 384

QY 41 AenlypPheTyrSerGlylscGlylscYsaArgGlylTyrCygsGlyValPro 56
DB 385 AACAGTCTACTGAGAGAGAGGTAGAGAGTACTGAGTGTCTCA 432

RESULT 5

US-10-361-997-58
Sequence 58, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 1965
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal
US-10-361-997-58

Alignment Scores:
Pred. No.: 1,238-39 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-58 (1-1965)

QY 1 GIUAIACyAaenleuprollevalargylprocygsllealaphhepProargtrpala 20
DB 1 GAGGCTGTACTGCAATGCGAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 60

QY 21 PheapAlaVallylgllylscCyvalleupheProTyrGlylCygsInglyangly 40
DB 61 TTCGATGCTGTAAGGTAAAGTGTGTTGTTCCCATAGGCTGTGTCAAGTAAAGGT 120

QY 41 AenlypPheTyrSerGlylscGlylscYsaArgGlylTyrCygsGlyValPro 56
DB 121 AACAGTCTACTGAGAGAGAGGTAGAGAGTACTGAGTGTCTCA 168

RESULT 6

US-10-361-997-60
Sequence 60, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 1965
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the C-terminal
US-10-361-997-60

Alignment Scores:
Pred. No.: 1,238-39 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-60 (1-1965)

QY 1 GIUAIACyAaenleuprollevalargylprocygsllealaphhepProargtrpala 20
DB 1798 GAGGCTGTACTGCAATGCGAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 1857

QY 21 PheapAlaVallylgllylscCyvalleupheProTyrGlylCygsInglyangly 40
DB 1858 TTCGATGCTGTAAGGTAAAGTGTGTTGTTCCCATAGGCTGTGTCAAGTAAAGGT 1917

QY 41 AenlypPheTyrSerGlylscGlylscYsaArgGlylTyrCygsGlyValPro 56
DB 1918 AACAGTCTACTGAGAGAGAGGTAGAGAGTACTGAGTGTCTCA 1965

RESULT 7

US-10-361-997-70
Sequence 70, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 3255
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: NotI cassette of pDB2300X2 with DX890 (Nterm) and
US-10-361-997-70

Alignment Scores:
Pred. No.: 2,388-39 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0

US-10-361-997-70

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-70 (1-3255)

QY 1 GUAACySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTTPala 20
DB 901 GAAGCTGTAACCTGCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 960

QY 21 PheAspAlaValAllyGlyCysValLeuPheProTyrGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTTAAGGTAAGGTGTTGTTCCCATATGAGGTGTCAGGTAAAGCT 1020

QY 41 AsnLysPheTyrSerGlnLysGluCysArgGlyTyrCysGlyValPro 56
DB 1021 AACAGTTCTACTCTGAAAAGATGTAGAGATATCTGAGGTTC 1068

RESULT 8
US-10-361-997-73
; Sequence 73, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 3440
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of NotI cassette of pDB2300X3 with 2
; OTHER INFORMATION: x DX-890
US-10-361-997-73

Alignment Scores:
Pred. No.: 2,466-39 Length: 3440
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-73 (1-3440)

QY 1 GUAACySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTTPala 20
DB 901 GAAGCTGTAACCTGCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 960

QY 21 PheAspAlaValAllyGlyCysValLeuPheProTyrGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTTAAGGTAAGGTGTTGTTCCCATATGAGGTGTCAGGTAAAGCT 1020

QY 41 AsnLysPheTyrSerGlnLysGluCysArgGlyTyrCysGlyValPro 56
DB 1021 AACAGTTCTACTCTGAAAAGATGTAGAGATATCTGAGGTTC 1068

RESULT 9
US-10-361-997-44
; Sequence 44, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000

; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DPL-14-(GGS)4 GG-RHA-(GGS)4-GG-DX-890 DNA sequence
US-10-361-997-44

Alignment Scores:
Pred. No.: 2,466-39 Length: 3444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-44 (1-3444)

QY 1 GUAACySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTTPala 20
DB 901 GAAGCTGTAACCTGCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 960

QY 21 PheAspAlaValAllyGlyCysValLeuPheProTyrGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTTAAGGTAAGGTGTTGTTCCCATATGAGGTGTCAGGTAAAGCT 1020

QY 41 AsnLysPheTyrSerGlnLysGluCysArgGlyTyrCysGlyValPro 56
DB 1021 AACAGTTCTACTCTGAAAAGATGTAGAGATATCTGAGGTTC 1068

RESULT 10
US-10-038-722-71
; Sequence 71, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8584
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid PHIL-D2 (MraI)pharePro::EPI-HNE-3) (Table 251)
US-10-038-722-71

Alignment Scores:
Pred. No.: 4,446-38 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0

DB: 16 Gaps: 0
US-10-038-722-27 (1-56) x US-10-038-722-71 (1-8584)
QY 2 AlaCysAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 1212 GCTGTACTTCCCAATCGTCAGAGTCATGCTCTTCTCCCAAGATGGGCTTTC 1271
QY 22 AspaIValIySGIlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAasnGlyAen 41
DB 1272 GACGCTGTAAAGGAGTAAGGCTCTTGTCCCAATACGGGAGTGTGTCAGTAACGGTAAAC 1331
QY 42 LysPheTySerGluLysGluCysArgGluTyrgGlyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGAGTACTGTGGTGTCCA 1376
RESULT 11
US-10-038-722-75
; Sequence 75, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 8590
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p02pick (MFAIphaPrePro::EPI-NHE-3) circular dedNA. (Table 253)
US-10-038-722-75
Alignment Scores:
Pred. No.: 4,45e-38 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
Gaps: 0
US-10-038-722-27 (1-56) x US-10-038-722-75 (1-8590)
QY 2 AlaCysAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 1212 GCTGTACTTCCCAATCGTCAGAGTCATGCTCTTCTCCCAAGATGGGCTTTC 1271
QY 22 AspaIValIySGIlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAasnGlyAen 41
DB 1272 GACGCTGTAAAGGAGTAAGGCTCTTGTCCCAATACGGGAGTGTGTCAGTAACGGTAAAC 1331
QY 42 LysPheTySerGluLysGluCysArgGluTyrgGlyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGAGTACTGTGGTGTCCA 1376
RESULT 12
US-10-298-796-27
; Sequence 27, Application US/10298796
; Publication No. US20030220490A1

; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-298-796-27
Alignment Scores:
Pred. No.: 8.01e-36 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
US-10-038-722-27 (1-56) x US-10-298-796-27 (1-204)
QY 2 AlaCysAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 4 GCTGTACTTCCCAATCGTCAGAGTCATGCTCTTCTCCCAAGATGGGCTTTC 63
QY 22 AspaIValIySGIlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAasnGlyAen 41
DB 64 GATGCTGTAAAGGAGTAAGGCTCTTCTTCCCAATACGGGAGTGTGTCAGTAACGGGAGTAAAC 123
QY 42 LysPheTySerGluLysGluCysArgGluTyrgGlyValPro 56
DB 124 AAGTCTACTCTGAGAGAGAGTGTAGAGAGTACTGTGGTGTCCA 168
RESULT 13
US-09-918-995-8710
; Sequence 8710, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8710
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-8710
Alignment Scores:
Pred. No.: 1.9e-35 Length: 408
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
US-10-038-722-27 (1-56) x US-09-918-995-8710 (1-408)
QY 2 AlaCysAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 218 GCTGTACTTCCCAATCGTCAGAGTCATGCTCTTCTCCCAAGATGGGCTTTC 277


```
Qy 22 AspaIaValIySGIyLYsCyVaIleuPheProTyRGlyGIyCyGInGIyAsnGIyAsn 41
Db 278 GATGCTGTCAGAGGGAGAGTGCCTCTTCCCTACGGGGGGCTGCACAGGGCAACGGGAAAC 337

Qy 42 LysPheTySerGIuLYsGIuCySaRgGIuTyRCySGIyValPro 56
Db 338 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 382

RESULT 14
US-10-298-796-28
; Sequence 28, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-298-796-28

Alignment Scores:
Pred. No.: 2,09e-35 Length: 441
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB: 17

US-10-038-722-27 (1-56) x US-10-298-796-28 (1-441)

Qy 2 AlaCySaNuLeuProIleValIaRgGIyProCySileAlaPheProArGTTPaIaPhe 21
Db 241 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 300

Qy 22 AspaIaValIySGIyLYsCyVaIleuPheProTyRGlyGIyCyGInGIyAsnGIyAsn 41
Db 301 GATGCTGTCAGAGGGAGAGTGCCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAAAC 360

Qy 42 LysPheTySerGIuLYsGIuCySaRgGIuTyRCySGIyValPro 56
Db 361 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 405

RESULT 15
US-10-291-265-214
; Sequence 214, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
/ SEQ ID NO 214
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
US-10-291-265-214

Alignment Scores:
Pred. No.: 7.85e-35 Length: 1280
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB: 17

US-10-038-722-27 (1-56) x US-10-291-265-214 (1-1280)

Qy 2 AlaCySaNuLeuProIleValIaRgGIyProCySileAlaPheProArGTTPaIaPhe 21
Db 958 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 1017

Qy 22 AspaIaValIySGIyLYsCyVaIleuPheProTyRGlyGIyCyGInGIyAsnGIyAsn 41
Db 1018 GATGCTGTCAGAGGGAGAGTGCCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAAAC 1077

Qy 42 LysPheTySerGIuLYsGIuCySaRgGIuTyRCySGIyValPro 56
Db 1078 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 1122
```

```
RESULT 16
US-09-978-418-7
; Sequence 7, Application US/09978418
; Publication No. US2003011897A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephan
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 142.US5.REG
; CURRENT APPLICATION NUMBER: US/09/978,418
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/311,305
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/314,734
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/318,204
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/326,470
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..263
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 264..926
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 927..1436
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1404..1409
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1421..1436
US-09-978-418-7
```

Alignment Scores: 9.06e-35 Length: 1436
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 10 Gaps: 0
DB: 10

US-10-038-722-27 (1-56) x US-09-978-418-7 (1-1436)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 1117 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1176

QY 22 AspaIaValIySGIlyVysCysValIeuPheProTyrgIyGlyCysGInGlyAsnGlyAsn 41
Db 1177 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1236

QY 42 LysPheTyrsSerGluIySGIlyCysArgIlyTyrgIyGlyValPro 56
Db 1237 AAGTTCCTACTCAGAGAGAGTGCAGAGTACTCGGCTGTCCT 1281

RESULT 17
US-09-925-301-333
Sequence 333, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 333
LENGTH: 1444
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-301-333

Alignment Scores: 9.12e-35 Length: 1444
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 9 Gaps: 0
DB: 9

US-10-038-722-27 (1-56) x US-09-925-301-333 (1-1444)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 1090 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1149

QY 22 AspaIaValIySGIlyVysCysValIeuPheProTyrgIyGlyCysGInGlyAsnGlyAsn 41
Db 1150 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1209

QY 42 LysPheTyrsSerGluIySGIlyCysArgIlyTyrgIyGlyValPro 56
Db 1210 AAGTTCCTACTCAGAGAGAGTGCAGAGTACTCGGCTGTCCT 1254

RESULT 18
US-10-291-265-686
Sequence 686, Application US/10291265
Patent No. US20030232054A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al

TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 686
LENGTH: 1464
TYPE: DNA
ORGANISM: Homo sapiens
US-10-291-265-686

Alignment Scores: 9.28e-35 Length: 1464
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 17 Gaps: 0
DB: 17

US-10-038-722-27 (1-56) x US-10-291-265-686 (1-1464)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 1143 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1202

QY 22 AspaIaValIySGIlyVysCysValIeuPheProTyrgIyGlyCysGInGlyAsnGlyAsn 41
Db 1203 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1262

QY 42 LysPheTyrsSerGluIySGIlyCysArgIlyTyrgIyGlyValPro 56
Db 1263 AAGTTCCTACTCAGAGAGAGTGCAGAGTACTCGGCTGTCCT 1307

RESULT 19
US-10-291-172-93
Sequence 93, Application US/10291172
Patent No. US20030228584A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO: 93
LENGTH: 1721
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (284)..(1339)
FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(1721)
OTHER INFORMATION: n = a,t,c or g
US-10-291-172-93

Alignment Scores:

Pred. No.: 1.13e-34 Length: 1721
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 17 Gaps: 0

US-10-038-722-27 (1-56) x US-10-291-172-93 (1-1721)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

DB 1139 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCATTT 1198

QY 22 AspaIaValIlysgIlylYsCysValIleupheProTyrgIyGlyCYsgInGIyAsnGIyAsn 41

DB 1199 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1258

QY 42 LysPheTySerGIuLyegIuCySaRgGIuTyrcYsgIyValPro 56

DB 1259 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1303

RESULT 20

US-10-221-278-93
Sequence 93, Application US/10221278
Publication No. US20040034208A1

GENERAL INFORMATION:

APPLICANT: HySeq, Inc
TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045
CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US/10/221,278

PRIOR FILING DATE: 2000-05-06

PRIOR APPLICATION NUMBER: 09/593,267

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/616,847

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 09/596,193

PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 752

SEQ ID NO 93

LENGTH: 1721

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS (1339)

LOCATION: (284)...(1339)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1721)

OTHER INFORMATION: n = a,t,c or g

US-10-221-278-93

Alignment Scores:

Pred. No.: 1.13e-34 Length: 1721

Score: 296.00 Matches: 51

Percent Similarity: 92.73% Conservative: 0

Best Local Similarity: 92.73% Mismatches: 4

Query Match: 89.97% Indels: 0

DB: 17 Gaps: 0

US-10-038-722-27 (1-56) x US-10-221-278-93 (1-1721)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

DB 1139 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCATTT 1198

QY 22 AspaIaValIlysgIlylYsCysValIleupheProTyrgIyGlyCYsgInGIyAsnGIyAsn 41

DB 1199 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1258

QY 42 LysPheTySerGIuLyegIuCySaRgGIuTyrcYsgIyValPro 56

DB 1259 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1303

RESULT 21

US-10-119-926-48
Sequence 48, Application US/10119926
Publication No. US20030104413A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Zhao, Qing A.

APPLICANT: Chen, Rui-hong

APPLICANT: Wehrman, Tom

APPLICANT: Zhou, Ping

APPLICANT: Xu, Chongjun

APPLICANT: Yang, Yonghong

APPLICANT: Xue, Aidong J.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20030104413A1el Nucleic Acids and

FILE REFERENCE: 789CIP2BCON

CURRENT APPLICATION NUMBER: US/10/119,926

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PC_Fl_genes Version 1.0

SEQ ID NO 48

LENGTH: 1781

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS (1402)

LOCATION: (344)...(1402)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1781)

OTHER INFORMATION: n = a,t,c or g

US-10-119-926-48

Alignment Scores:

Pred. No.: 1.18e-34 Length: 1781

Score: 296.00 Matches: 51

Percent Similarity: 92.73% Conservative: 0

Best Local Similarity: 92.73% Mismatches: 4

Query Match: 89.97% Indels: 0

DB: 15 Gaps: 0

US-10-038-722-27 (1-56) x US-10-119-926-48 (1-1781)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

DB 1199 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCATTT 1258

QY 22 AspaIaValIlysgIlylYsCysValIleupheProTyrgIyGlyCYsgInGIyAsnGIyAsn 41

DB 1259 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1318

QY 42 LysPheTySerGIuLyegIuCySaRgGIuTyrcYsgIyValPro 56

Db 1319 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 1363

RESULT 22

US-09-918-995-30403

Sequence 30403, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30403

LENGTH: 512

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(512)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-30403

Alignment Scores:

Pred. No.: 4,9e-33 Length: 512

Score: 281.00 Matches: 49

Percent Similarity: 89.09% Conservative: 0

Best Local Similarity: 89.09% Mismatches: 6

Query Match: 85.41% Indels: 0

DB: 10 Gaps: 0

US-10-038-722-27 (1-56) x US-09-918-995-30403 (1-512)

QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrpAlaPhe 21

Db 339 GCTTCATCTCCCATAGTCCGGGGCCCTCCGAGCTTATCCAGCTCTGGGCATTT 388

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 389 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACCGGAAC 448

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 449 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 493

RESULT 23

US-09-918-995-31769

Sequence 31769, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31769

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(466)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-31769

Alignment Scores:

Pred. No.: 1.78e-32 Length: 466

Score: 277.00 Matches: 49

Percent Similarity: 89.09% Conservative: 0

Best Local Similarity: 89.09% Mismatches: 6

Query Match: 84.19% Indels: 0

DB: 10 Gaps: 0

US-10-038-722-27 (1-56) x US-09-918-995-31769 (1-466)

QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrpAlaPhe 21

Db 229 GCTTCATCTCCCATAGTCCGGGGCCCTCCGAGCTTATCCAGCTCTGGGCATTT 288

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 289 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACCGGAAC 348

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 349 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 393

RESULT 24

US-09-960-352-4435

Sequence 4435, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengping

APPLICANT: Byatt, John C.

APPLICANT: Mathiasagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 4435

LENGTH: 435

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 19-LTB34-040-Q1-E1-E3

US-09-960-352-4435

Alignment Scores:

Pred. No.: 2.72e-31 Length: 435

Score: 269.00 Matches: 44

Percent Similarity: 89.29% Conservative: 6

Best Local Similarity: 78.57% Mismatches: 6

Query Match: 81.76% Indels: 0

DB: 9 Gaps: 0

US-10-038-722-27 (1-56) x US-09-960-352-4435 (1-435)

QY 1 GluAlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrpAla 20

Db 136 GAGGCTGTAACTCCCATAGTCCAGGGGCGCATGCCAGAGTATCCAGCTCTGGGCA 195

QY 21 PheAspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40

Db 196 TTTATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAATGCT 255

QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 256 AACAAATTTACTCGAGAGAGAGTGAAGAGTACTGCGATTCCT 303

RESULT 25

US-10-322-281-271/C

Sequence 271, Application US/10322281

Publication No. US20040126762A1

GENERAL INFORMATION:

```

APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 271
LENGTH: 120239
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(120239)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-271

```

Alignment Scores:

Pred. No.:	4.9e-27	Length:	10239
Score:	261.00	Matches:	43
Percent Similarity:	87.27%	Conservative:	5
Best Local Similarity:	78.18%	Mismatches:	7
Query Match:	79.33%	Indels:	0
DB:	18	Gaps:	0

US-10-038-722-27 (1-56) x US-10-322-281-271 (1-120239)

Accession	Protein	Length	Score	E-value
Oy	2.1a3cysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTPALaPhe	21	11.1	1.1e-05
Db	120205 GCCTGCATCTCCCATTAAGCCCTGCGAGCCTTCATAAAGCTCTGGCATTT	120146		
Oy	22 AspaIaValIyGlyIyCysValIleuPheProTyrGlyIyCysGlnIyAsnGlyAan	41	11.1	1.1e-05
Db	120145 GATTCAGCACAAGGGAAGTGCATTCATTCACATCGAGGGGGCTGCAAGAAGCAGCGGCAAC	120086		
Oy	42 LysPheTyrSerGluIyGlyCysArgIuTyrCysGlyValPro	56	11.1	1.1e-05
Db	120085 AAATCTCTCTCGAGAGGAATGCAAGAAGTCTCTGGAGAGTCCCT	120041		

Search completed: February 23, 2005, 06:34:28
Job time : 1784 secs

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCBP060"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 2.23e-28 Length: 383
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV696152 (1-383)

QY 2 AAlaCysAenLeuProIleValArgIyProCysIleAlaPhePheProArgTrpAlaPhe 21
|||||
DB 56 GCTTCATCTCCCATAGTCCGGGCCCCCTCCGAGCCTTCATCCAGCTCGGCATT 115
|||||

QY 22 AaPaIaValIyGlyLyCySeValIeuPheProTyrgIyGlyCyGInglyAaNglyAa 41
|||||
DB 116 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 175
|||||

QY 42 LysPheTySerGluLyGluCyAaGluTyrgIyGlyValPro 56
|||||
DB 176 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 220
|||||

RESULT 2

LOCUS AV686452 387 bp mRNA linear EST 16-JAN-2002
DEFINITION AV686452 GKC Homo sapiens cDNA clone GKAEF08 5', mRNA sequence.
ACCESSION AV686452
VERSION AV686452.1 GI:10288315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 387)
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Pu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL MEDLINE PUBLISHED
21625106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source 1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCBP08"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GKC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 2.26e-28 Length: 387
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV686452 (1-387)

QY 2 AAlaCysAenLeuProIleValArgIyProCysIleAlaPhePheProArgTrpAlaPhe 21
|||||
DB 57 GCTTCATCTCCCATAGTCCGGGCCCCCTCCGAGCCTTCATCCAGCTCGGCATT 116
|||||

QY 22 AaPaIaValIyGlyLyCySeValIeuPheProTyrgIyGlyCyGInglyAaNglyAa 41
|||||
DB 117 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 176
|||||

QY 42 LysPheTySerGluLyGluCyAaGluTyrgIyGlyValPro 56
|||||
DB 177 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 221
|||||

RESULT 3

LOCUS AV657651 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV657651 GLC Homo sapiens cDNA clone GLCFB05 3', mRNA sequence.
ACCESSION AV657651
VERSION AV657651.1 GI:9878665
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 394)
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Pu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL MEDLINE PUBLISHED
21625106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source 1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCFB05"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 2.31e-28 Length: 394
Score: 296.00 Matches: 51

Percent Similarity: 92.73%
 Best Local Similarity: 92.73%
 Query Match: 89.97%
 DB: 1
 Gaps: 0

US-10-038-722-27 (1-56) x AV657651 (1-394)

QY 2 AlaCysaenleuproillevalarglyProCysillealaphpheProargTrpAlaPhe 21
 Db 67 GCTGCATCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 126
 QY 22 AspaIaVallyGlyVlyGlyCysValleupheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 Db 127 GATGCTGCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCACAGGCAACGGAAC 186
 QY 42 LysPheTyrsenGlyVlyGlyCysArgGlyTyrCysGlyValPro 56
 Db 187 AAGTCTACTCAGAGAGAGTGCAGAGATCTGCGGTCTCT 231

RESULT 4

LOCUS AV656508 417 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV656508 GLC Homo sapiens cDNA clone GLCESA11 3', mRNA sequence.
 VERSION AV656508
 KEYWORDS AV656508.1 GI:987522
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 417)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

21625106
 MEDLINE
 PUBMED
 11752456
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

1..417
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCESA11"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GLC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e-28 Length: 417
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV656508 (1-417)

QY 2 AlaCysaenleuproillevalarglyProCysillealaphpheProargTrpAlaPhe 21
 Db 88 GCTGCATCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 147

QY 22 AspaIaVallyGlyVlyGlyCysValleupheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 Db 148 GATGCTGCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCACAGGCAACGGAAC 207

QY 42 LysPheTyrsenGlyVlyGlyCysArgGlyTyrCysGlyValPro 56
 Db 208 AAGTCTACTCAGAGAGAGTGCAGAGATCTGCGGTCTCT 252

RESULT 5

LOCUS AV695187 417 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV695187 GKC Homo sapiens cDNA clone GKCBC01 5', mRNA sequence.
 VERSION AV695187
 KEYWORDS AV695187.1 GI:10297050
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 417)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

21625106
 MEDLINE
 PUBMED
 11752456
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

1..417
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKCBC01"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e-28 Length: 417
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV695187 (1-417)

QY 2 AlaCysaenleuproillevalarglyProCysillealaphpheProargTrpAlaPhe 21
 Db 95 GCTGCATCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 154

QY 22 AspaIaVallyGlyVlyGlyCysValleupheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 Db 155 GATGCTGCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCACAGGCAACGGAAC 214

Oy 42 LysPheTYrSerGIuLyGluCySArgIuTYrCYGlyValPro 56
 Db 215 AAGTCTACTCAGAGAAGAGTGCAGAGACTACTCGGTGTCCT 259
 RESULT 6
 LOCUS AV682129 449 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV682129 GKB Homo sapiens cDNA clone GKBADJ06 5', mRNA sequence.
 ACCESSION AV682129
 VERSION AV682129.1 GI:10283392
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 449)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 JOURNAL 21625106
 MEDLINE 11752456
 PUBMED
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@hgsc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
 source
 1..449
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKBADJ06"
 /issue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_1ib="GKB"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,72e-28 Length: 449
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 Gaps: 0
 DB: 1
 US-10-038-722-27 (1-56) x AV682129 (1-449)
 Oy 2 AAlaCySAsnLeuProIleValAlaGlyProCYsIleAlaPhePheProArgTTPAlaPhe 21
 Db 122 GCCTGCATCTCCCATAGTCGGGGGCCCTGCGAGCCTTTCAGACTCGGGCATTT 181
 Oy 22 AApAlaValLyGlyLyCySValLeuPheProTYrGlyGlyCYGlnGlyAsnGlyAen 41
 Db 182 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTTAAGGGGGCTGCCAGGGCAACGGGAAC 241
 Oy 42 LysPheTYrSerGIuLyGluCySArgIuTYrCYGlyValPro 56
 Db 242 AAGTCTACTCAGAGAAGAGTGCAGAGACTACTCGGTGTCCT 286
 RESULT 7
 A1114613

LOCUS A1114613 450 bp mRNA linear EST 11-NOV-1999
 DEFINITION HAI200 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION A1114613
 VERSION A1114613.1 GI:6359958
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 450)
 Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
 and He, F.
 Expression profile analysis of a human fetal liver cDNA library
 and He, F.
 TITLE Unpublished (1998)
 JOURNAL Contact: Yongtao Yu
 COMMENT Department of Hematology
 Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing 100850, P.R.China
 Tel: 0086-10-68159479
 Fax: 0086-10-68214653
 Email: ytyf48@yahoo.com.
 FEATURES
 source
 1..450
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /issue_type="liver"
 /dev_stage="fetal"
 /lab_host="WC1061/P3"
 /clone_1ib="Human fetal liver cDNA library"
 /note="Vector: pCDNA1"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,73e-28 Length: 450
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 Gaps: 0
 DB: 1
 US-10-038-722-27 (1-56) x A1114613 (1-450)
 Oy 2 AAlaCySAsnLeuProIleValAlaGlyProCYsIleAlaPhePheProArgTTPAlaPhe 21
 Db 120 GCCTGCATCTCCCATAGTCGGGGGCCCTGCGAGCCTTTCAGACTCTGGGCATTT 179
 Oy 22 AApAlaValLyGlyLyCySValLeuPheProTYrGlyGlyCYGlnGlyAsnGlyAen 41
 Db 180 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTTAAGGGGGCTGCCAGGGCAACGGGAAC 239
 Oy 42 LysPheTYrSerGIuLyGluCySArgIuTYrCYGlyValPro 56
 Db 240 AAGTCTACTCAGAGAAGAGTGCAGAGACTACTCGGTGTCCT 284
 RESULT 8
 A1246161/c
 LOCUS A1246161 487 bp mRNA linear EST 28-JAN-1999
 DEFINITION q129b06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1857875
 3' similar to gb:X04225 ALPHA-1-MICROGLOBULIN (HUMAN);, mRNA
 sequence.
 ACCESSION A1246161
 VERSION A1246161.1 GI:3841558
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 487)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtmail.nih.gov

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 511 Std Error: 0.00
Seq primer: -40UP from Gldco

High quality sequence stop: 331.
Location/Qualifiers

FEATURES
source

```
1..487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1857875"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_1lb="Soares NHPu S1"
/notes="Organ: mixed (see below); Vector: pTT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHM, pregnant uterus
NHPu, and fetal heart NHPu19W) were mixed, and 88 circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."
```

ORIGIN

Alignment Scores:

Pred. No.:	3,02e-28	Length:	487
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1246161 (1-487)

```
Oy 2 AlaCyAenLeuProIleValaIaRgLyProCyAllealaphheProArGTpAlaPhe 21
Db 316 GCGTCGATCTCCCATATGTCGGGGCCCTCGAGCCTTCATCAGCTCGGCATT 257
Oy 22 AspaIaValLySGLyLyCyVaIleuPheProTyRgLyLyCySGInGlyAaNGIyAa 41
Db 256 GATGCTGTCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCCAGGGCAACCGGAAC 197
Oy 42 LysPheTyRserGluLySGLyCyAaRgLyLyTyRyCySGIyValPro 56
Db 196 AAGTTCTACTCAGAGAGAGTGCAGAGATCTCGGATGCCCT 152
```

RESULT 9

AV720273/c

LOCUS AV720273 520 bp mRNA linear EST 16-OCT-2000

DEFINITION AV720273 GLC Homo sapiens cDNA clone GLCBA03 5', mRNA sequence.

ACCESSION AV720273

VERSION AV720273.1 GI:10817425

KEYWORDS

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

Qian, B., Wu, T., Huang, Q., Kang, B., Gao, X., Xu, Z.,
Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z.,
Zeng, L., Xu, S., Gu, Y., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Yang, Y., Gu, Y., Chen, Z., and Han, Z.

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source

```
1..520
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCBA03"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1lb="GLC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
```

ORIGIN

Alignment Scores:

Pred. No.:	3.28e-28	Length:	520
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV720273 (1-520)

```
Oy 2 AlaCyAenLeuProIleValaIaRgLyProCyAllealaphheProArGTpAlaPhe 21
Db 317 GCGTCGATCTCCCATATGTCGGGGCCCTCGAGCCTTCATCAGCTCGGCATT 258
Oy 22 AspaIaValLySGLyLyCyVaIleuPheProTyRgLyLyCySGInGlyAaNGIyAa 41
Db 257 GATGCTGTCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCCAGGGCAACCGGAAC 198
Oy 42 LysPheTyRserGluLySGLyCyAaRgLyLyTyRyCySGIyValPro 56
Db 197 AAGTTCTACTCAGAGAGAGTGCAGAGATCTCGGATGCCCT 153
```

RESULT 10

A1333042/c

LOCUS A1333042 525 bp mRNA linear EST 13-FEB-1999

DEFINITION q931h04.x1 Soares NHPu S1 Homo sapiens cDNA clone IMAGE:1934167
3' similar to gb:X04225 ALPBA-1-MICROGLOBULIN (HUMAN);, mRNA
sequence.

ACCESSION

A1333042

VERSION A1333042.1 GI:4069601

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-rtmail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1327 Std Error: 0.00

Seq primer: -40UP from Gldco

High quality sequence stop: 410.

Location/Qualifiers

1..525

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1934167"

/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soareg_NHMPU_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBH19M) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:

Pred. No.:	3.32e-28	Length:	525
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1333042 (1-525)

QY 2 A1ACyAaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrpAlaPhe 21

DB 337 GCTTCATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTTTGGGCAATT 278

QY 22 AspaIaValIyGlyCySValIleuPheProTyGlyGlyCyGlnGlyAaenGlyAaen 41

DB 277 GATGCTGTCAAGGGAAGAGTGGCTCTCTTCCCTACGGGGGCTGCCAGGCAACGGGAAC 218

QY 42 LysPheTySerGlyIyGlyCySArgGlyIyTyCyGlyValPro 56

DB 217 AAGTTTACTCAGAGAGAGTGCAGAGTACTGGGTCCT 173

RESULT 11

LOCUS AV654685 535 bp mRNA linear EST 15-JAN-2002

DEFINITION AV654685 GUC Homo sapiens cDNA clone GLCDYD11 3', mRNA sequence.

ACCESSION AV654685.1 GI:9875699

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21625106

COMMENT 11752456

CONTACT: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

1..535
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="GLCDYD11"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOAR"
/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	3.4e-28	Length:	535
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV654685 (1-535)

QY 2 A1ACyAaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrpAlaPhe 21

DB 127 GCTTCATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTTTGGGCAATT 186

QY 22 AspaIaValIyGlyCySValIleuPheProTyGlyGlyCyGlnGlyAaenGlyAaen 41

DB 187 GATGCTGTCAAGGGAAGAGTGGCTCTCTTCCCTACGGGGGCTGCCAGGCAACGGGAAC 246

QY 42 LysPheTySerGlyIyGlyCySArgGlyIyTyCyGlyValPro 56

DB 247 AAGTTTACTCAGAGAGAGTGCAGAGTACTGGGTCCT 291

RESULT 12

LOCUS CB144250 543 bp mRNA linear EST 29-JAN-2003

DEFINITION K-EST0198507 L7N80010281 Homo sapiens cDNA clone L7N80010281-22-F06

ACCESSION CB144250

VERSION CB144250.1 GI:28122110

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4409

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 22 row: F column: 06

High quality sequence stop: 543.

FEATURES

1..543
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N80010281-22-F06"
/sex="M"
/lab_host="Top10F"
/clone_lib="L7N80010281"
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tabacco acid pyrophosphatase (TAP). The deacapped intact mRNA was ligated with DNA-RNA linker including

ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcorI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and Nid114 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F⁺ with electroporation method."

ORIGIN

Alignment Scores:

Pred. No.: 3,466-28
Percent Similarity: 296.00
Best Local Similarity: 92.73%
Query Match: 92.73%
DB: 89.97%

Length: 543
Matches: 51
Conservative: 0
Mismatches: 4
Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x CB144250 (1-543)

QY 2 AlaCysAsnLeuProIleValaArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 319 GCGTCAATCTCCCATAGTCCGGGGCCCTCCAGCCTTCATCCAGCTCGGCAATT 378
QY 22 AapAlaValAllyGlyLysCysValLeuPheProTyrGlyGlyGlnGlyAsnGlyAsn 41
DB 379 GATGCTGTCAGAGGAGAGTGGCTCTCTCCCTACGGGGGCTGCGCAGGGCAACGGAAC 438
QY 42 LysPheTyrSerGlyLysGlyLysCysArgGlyLysGlyValPro 56
DB 439 AAGTCTACTCTCAGAGAGAGTGCAGAGAGTACTGCGGTGCTCCT 483

RESULT 13

CB148803 543 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0205202 L7N800102s1 Homo sapiens cDNA clone L7N800102s1-21-B07
DEFINITION 5', mRNA sequence.

ACCESSION CB148803
VERSION CB148803.1 GI:28131454
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 543)
AUTHORS Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, K.J., Cheong, D.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong, Yuseong-gu, Daejeon 305-335, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

Plate: 21 row: B column: 07
High quality sequence stop: 543.
Location/Qualifiers
1. 543

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N800102s1-21-B07"
/sex="M"
/lab_host="Top10F"
/clone_lib="L7N800102s1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcorI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tobacco acid pyrophosphatase (TAP). The deacapped intact mRNA was ligated with DNA-RNA linker including EcorI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcorI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and Nid114 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F⁺ with electroporation method."

ORIGIN

Alignment Scores:

Pred. No.: 3,466-28
Percent Similarity: 296.00
Best Local Similarity: 92.73%
Query Match: 92.73%
DB: 89.97%

Length: 543
Matches: 51
Conservative: 0
Mismatches: 4
Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x CB148803 (1-543)

QY 2 AlaCysAsnLeuProIleValaArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 319 GCGTCAATCTCCCATAGTCCGGGGCCCTCCAGCCTTCATCCAGCTCGGCAATT 378
QY 22 AapAlaValAllyGlyLysCysValLeuPheProTyrGlyGlyGlnGlyAsnGlyAsn 41
DB 379 GATGCTGTCAGAGGAGAGTGGCTCTCTCCCTACGGGGGCTGCGCAGGGCAACGGAAC 438
QY 42 LysPheTyrSerGlyLysGlyLysCysArgGlyLysGlyValPro 56
DB 439 AAGTCTACTCTCAGAGAGAGTGCAGAGAGTACTGCGGTGCTCCT 483

RESULT 14

AI193912 550 bp mRNA linear EST 29-OCT-1998
LOCUS AI193912.1
DEFINITION qe73b01.x1 Soares fetal lung Nblh19w Homo sapiens cDNA clone IMAGE:1744585 3' similar to gb:X04225 ALPBA-1-MICROGLOBULIN (HUMAN); mRNA sequence.
ACCESSION AI193912
VERSION AI193912.1 GI:3745121
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 643 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 337.
Location/Qualifiers
1..550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1744585"
/dev_stage="19 weeks"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung NBHL19W"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTCACATCTGAGATGAGAGGAGGCGCCCATTTTCTTTTCTTTT-3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."

ORIGIN

Alignment Scores:
Pred. No.: 3,52e-28 Length: 550
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x A1193912 (1-550)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCyAlleAlaPhePheProArgTrpAlaPhe 21
Db 316 GCGTGAATCTCCCATATGTCGGGGCCCTGCGAGCCTTATCCAGCTCGGCAATT 257

QY 22 AspAlaValIlyGlyLysCyValLeuPheProTyrGlyGlyCyGlnGlyAangIyAan 41
Db 256 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGAGGGGGCTGCAGGGCAACGGGAAC 197

QY 42 LysPheTyrSerGluLysGlyCyAangIyLysCyGlnGlyValPro 56
Db 196 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 152

RESULT 15
A1207590/c 571 bp mRNA linear EST 11-NOV-1999
LOCUS A1207590 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
DEFINITION Ha2594 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
sequence.
ACCESSION A1207590
VERSION A1207590.1 GI:6361600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 571)
AUTHORS Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
and He, F.
TITLE Expression profile analysis of a human fetal liver cDNA library
JOURNAL Unpublished (1998)
COMMENT Contact: Chenggang Zhang
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Email: zhang_chenggang@hotmail.com.
Location/Qualifiers
1..571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/P3"
/clone_lib="Human fetal liver cDNA library"
/note="Vector: pCDNA1"

ORIGIN

Alignment Scores:
Pred. No.: 3,69e-28 Length: 571
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x A1207590 (1-571)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCyAlleAlaPhePheProArgTrpAlaPhe 21
Db 316 GCGTGAATCTCCCATATGTCGGGGCCCTGCGAGCCTTATCCAGCTCGGCAATT 257

QY 22 AspAlaValIlyGlyLysCyValLeuPheProTyrGlyGlyCyGlnGlyAangIyAan 41
Db 256 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGAGGGGGCTGCAGGGCAACGGGAAC 197

QY 42 LysPheTyrSerGluLysGlyCyAangIyLysCyGlnGlyValPro 56
Db 196 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 152

RESULT 16
A1336247/c 583 bp mRNA linear EST 13-FEB-1999
LOCUS A1336247 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone
DEFINITION q45b07.x1 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone
IMAGE:1950901.3' similar to gp:X04225 ALPFA-1-WICKROGLOBULIN
(HUMAN);, mRNA sequence.
ACCESSION A1336247
VERSION A1336247.1 GI:4073174
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 833 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 297.
Location/Qualifiers
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:1950901"
/dev stage="19 weeks"
/lab host="DH10B (ampicillin resistant)"
/clone.lib="Soares fetal lung NBH19W"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT-3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBH19W."

ORIGIN

Alignment Scores:

Pred. No.:	3,79e-28	Length:	583
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1336247 (1-583)

QY 2 A1aCysaenLeuProIleValArgIyProCySilllealaphPheProArgTTPalphe 21
Db 319 GCTTCACATCTCCCATATGTCGGGGCCCTGCGCAGCCTTCATCCAGCTTGCGCATTT 260
QY 22 AapAlaValLySGLyLysCySValLeuPheProTyrGlyGlyCySGInGlyAsnGlyAsn 41
Db 259 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGCGGGGCTGCGCAGCGGCAACGGAAC 200
QY 42 LysPheTyrSerGlyLysGlyLysCySArgIyTyrCySGIyValPro 56
Db 199 AAGTTTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 155

RESULT 17
LOCUS AV683002 617 bp mRNA linear EST 16-JAN-2002
DEFINITION AV683002 GKC Homo sapiens cDNA clone GKCBB06 5', mRNA sequence.
ACCESSION AV683002
VERSION AV683002.1 GI:10284865
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 617)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL MEDLINE
PUBMED 21625106

COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..617
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCBB06"
/tissue_type="hepatocellular carcinoma"
/dev stage="adult"
/lab host="SOAR"
/clone.lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	4.07e-28	Length:	617
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV683002 (1-617)

QY 2 A1aCysaenLeuProIleValArgIyProCySilllealaphPheProArgTTPalphe 21
Db 59 GCTTCACATCTCCCATATGTCGGGGCCCTGCGCAGCCTTCATCCAGCTTGCGCATTT 118
QY 22 AapAlaValLySGLyLysCySValLeuPheProTyrGlyGlyCySGInGlyAsnGlyAsn 41
Db 119 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGCGGGGCTGCGCAGCGGCAACGGAAC 178
QY 42 LysPheTyrSerGlyLysGlyLysCySArgIyTyrCySGIyValPro 56
Db 179 AAGTTTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 223

RESULT 18
LOCUS A1807643 644 bp mRNA linear EST 19-DEC-1999
DEFINITION w149d04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2358919 3' similar to gb:X04225 ALPBA-1-MICROGLOBULIN (HUMAN); mRNA sequence.
ACCESSION A1807643
VERSION A1807643.1 GI:5394209
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 644)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
This clone is available royally-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1328 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 462.

FEATURES

source
1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2358919"
/lab host="DH10B"
/clone.lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19W, testis NHR, and B-cell NCI-GAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731359. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	4,296-28	Length:	644
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1807643 (1-644)

QY 2 A1ACyAsnLeuProIleValArgIyProCyAlleAlaPhePheProArgTIPAlaPhe 21

Db 313 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCTGGGCATT 254

QY 22 AspAlaValIyGlyIyCySValIleuPheProTyrGlyIyCyGInglYAsnGlyAsn 41

Db 253 GATGCTGCAGGGAGAGTGTCTCTCTCCCTACGGGGGCTGCGAGGCAACGGAGAC 194

QY 42 LysPheTyrSerGlyIyGlyCySArgIyTyrCySGLYValPro 56

Db 193 AAGTCTACTCAGAGAGAGTGCAGAGAGTCTCGCGTCTCCT 149

RESULT 19

AV686492 670 bp mRNA linear EST 16-JAN-2002

LOCUS AV686492 GKC Homo sapiens cDNA clone GKCNF08 5', mRNA sequence.

DEFINITION AV686492.1 GI:10288355

VERSION AV686492.1 GI:10288355

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 670)

AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,

TITLE Insight into hepatocellular carcinogenesis at transcriptome level

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

COMMENT Contact: Zeguang Han

MEDLINE Chinese National Human Genome Center at Shanghai

PUBMED 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

FEATURES

source

1..670

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="GKCNF08"

/issue_type="hepatocellular carcinoma"

/dev_host="Adult"

/lab_host="SOLR"

/clone_lib="GKC"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-038-722-27 (1-56) x AV686492 (1-670)

QY 2 A1ACyAsnLeuProIleValArgIyProCyAlleAlaPhePheProArgTIPAlaPhe 21

Db 95 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCTGGGCATT 154

QY 22 AspAlaValIyGlyIyCySValIleuPheProTyrGlyIyCyGInglYAsnGlyAsn 41

Db 155 GATGCTGCAGGGAGAGTGTCTCTCTCCCTACGGGGGCTGCGAGGCAACGGAGAC 214

QY 42 LysPheTyrSerGlyIyGlyCySArgIyTyrCySGLYValPro 56

Db 215 AAGTCTACTCAGAGAGAGTGCAGAGAGTCTCGCGTCTCCT 259

RESULT 20

AW173259/c 675 bp mRNA linear EST 16-NOV-1999

LOCUS AW173259/c

DEFINITION XJ55C08.x1 Soares NFI, T GBC S1 Homo sapiens cDNA clone

VERSION IMAGE:2664014.3' similar to gb:X04225 ALPFA-1-MICROGLOBULIN

KEYWORDS (HUMAN); mRNA sequence.

SOURCE AW173259.1 GI:6439207

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 675)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Contact: Robert Strausberg, Ph.D.

MEDLINE Email: cga@bcr.tnml.nih.gov

PUBMED This clone is available royalty-free through LNL; contact the

FEATURES

source

1..675

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="IMAGE:2664014"

/lab_host="BDH10B"

/clone_lib="Soares_NFI_T_GBC_S1"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NBHL9W, testis NHT, and B-cell

NCI-CGAP GCBI) were mixed and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

726408-728711, and 729096-731359. Subtraction by Bento

Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-038-722-27 (1-56) x AV686492 (1-670)

QY 2 A1ACyAsnLeuProIleValArgIyProCyAlleAlaPhePheProArgTIPAlaPhe 21

Db 95 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCTGGGCATT 154

QY 22 AspAlaValIyGlyIyCySValIleuPheProTyrGlyIyCyGInglYAsnGlyAsn 41

Db 155 GATGCTGCAGGGAGAGTGTCTCTCTCCCTACGGGGGCTGCGAGGCAACGGAGAC 214

QY 42 LysPheTyrSerGlyIyGlyCySArgIyTyrCySGLYValPro 56

Db 215 AAGTCTACTCAGAGAGAGTGCAGAGAGTCTCGCGTCTCCT 259

Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AM173259 (1-675)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 312 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCGGGCATTT 253

QY 22 AApAlaValIlyGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 252 GATGCTGTCAAGGGAGAGTGCCTCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 193

QY 42 LysPheTyrSerGluTylGlyGluCysArgGluTyrCysGlyValPro 56
DB 192 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCTCT 148

RESULT 21
AV686493 682 bp mRNA linear EST 16-JAN-2002
LOCUS AV686493 GKC Homo sapiens cDNA clone GKCENF09 5', mRNA sequence.
DEFINITION AV686493
ACCESSION AV686493.1 GI:10288356
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 682)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCENF09"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores: 4.62e-28 Length: 682
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 4
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 1 Gaps: 0
US-10-038-722-27 (1-56) x AV686493 (1-682)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 312 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCGGGCATTT 253

DB 95 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCGGGCATTT 154

QY 22 AApAlaValIlyGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 155 GATGCTGTCAAGGGAGAGTGCCTCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 214

QY 42 LysPheTyrSerGluTylGlyGluCysArgGluTyrCysGlyValPro 56
DB 215 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCTCT 259

RESULT 22
AV645324 683 bp mRNA linear EST 15-JAN-2002
LOCUS AV645324 GUA Homo sapiens cDNA clone GLAAB01 3', mRNA sequence.
DEFINITION AV645324
ACCESSION AV645324.1 GI:9866338
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 683)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAB01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GUA"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores: 4.62e-28 Length: 683
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 1 Gaps: 0
US-10-038-722-27 (1-56) x AV645324 (1-683)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 296 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCCAGCTCGGGCATTT 237

QY 22 AApAlaValIlyGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 236 GATGCTGTCAAGGGAGAGTGCCTCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 177

QY 42 LysPheTyrSerGluTylGlyGluCysArgGluTyrCysGlyValPro 56

[illegible]

ACCESSION	AV645372
VERSION	AV645372.1
KEYWORDS	GI:9866386
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 692)
JOURNAL	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
MEDLINE	Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
PUBMED	Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
COMMENT	Hu,G., Gu,J., Chen,Z. and Han,Z.
	Insight into hepatocellular carcinogenesis at transcriptome level
	by comparing gene expression profiles of hepatocellular carcinoma
	with those of corresponding noncancerous liver
	21625106
	Proc.Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
	11752456
	Contact: Zeguang Han
	Chinese National Human Genome Center at Shanghai
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
	201203, P. R. China
	Tel: 86-21-50801919 (ex.45)
	Fax: 86-21-50801922
	Email: hanzg@chgc.sh.cn
	This clone is available at CHGC in Shanghai.
FEATURES	Location/Qualifiers
source	1..692
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="G1AAAF01"
	/tissue_type="corresponding non cancerous liver tissue"
	/dev_stage="Adult"
	/lab_host="SOIR"
	/clone_lib="G1A"
	/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
	XhoI"
ORIGIN	
Alignment Scores:	
Pred. No.:	4.7e-28
Score:	296.00
Percent Similarity:	92.73%
Best Local Similarity:	92.73%
Query Match:	89.97%
DB:	1
	Gaps: 0
US-10-038-722-27 (1-56) x AV645372 (1-692)	
OY	2
Db	297
OY	22
Db	237
OY	42
Db	177
RESULT 25	
LOCUS	B0689265/c
DEFINITION	692 bp mRNA linear EST 07-OCT-2002
ACCESSION	B0689265
VERSION	EST
KEYWORDS	EST
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 692)
Ronald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

Location/Qualifiers
1..692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-ECL-adv-b-01-0-UI"
/tissue_type="lung"
/dev_stage="Adult and Fetal"
/lab_host="PHIOB (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-ECL"
/note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-ECL is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Ronald, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pTT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-ECL
TAG_SEQ=AAGTGGCTTAC"

ORIGIN

Alignment Scores:
Pred. No.: 4.7e-28 Length: 692
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 5 Gaps: 0

US-10-038-722-27 (1-56) x BUE69265 (1-692)

QY 2 AAlaCyAsmLeuProIlleValArgGlyProCySileAlaPhePheProArgTrrAlaPhe 21
DB 331 GCGTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCAGCTCGGGCATTT 272
QY 22 AspAlaValLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 271 GATGCTGTCAAGGGAAGTGCCTCTCCCTACGGGGGCTGCAGGGCAACGGGAAC 212

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 211 AAGTCTACTCAGAGAAAGAGTGCAGAGACTGCGGGTCCCT 167

Search completed: February 23, 2005, 06:02:16
Job time : 2307 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 04:19:32 ; Search time 138 Seconds

(without alignments)
663.996 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPIVRCGICAFPPRWA.....QGNGKFKYSEKREYCGVP 56

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh

-O=/cgn2_1/USPTO.spool/US10038722/runat_18022005_145236_14347/app_query_fastq_1.139

-DB=Issued_Patents_NA -QMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi

-LIST=45 -DOCALIGN=200 -THR MAX=100 -THR MIN=0 -ALIGN=25

-MODE=LOCAL -OUTFMT=pcio -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10038722 @CGN 1 1 1177 @runat_18022005_145236_14347 -NCPU=6 -ICPU=3

-NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6

-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/1/ina/6C.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	448	1	US-08-358-160-66
2	324	98.5	8584	1	US-08-358-160-66
3	324	98.5	8590	1	US-08-358-160-70
4	296	90.0	198	1	US-07-791-213D-12
5	296	90.0	198	1	US-08-293-150A-12
6	296	90.0	204	4	US-09-331-793-27
7	296	90.0	204	4	US-07-791-213D-15
8	296	90.0	209	1	US-08-293-150A-15
9	296	90.0	210	1	US-07-791-213D-11
10	296	90.0	210	1	US-07-972-387-74
11	296	90.0	210	1	US-08-431-412-74
12	296	90.0	210	1	US-08-057-971-74

13	296	90.0	210	1	US-08-293-150A-11	Sequence 11, Appl
14	296	90.0	210	2	US-08-235-515A-24	Sequence 24, Appl
15	296	90.0	295	1	US-07-791-213D-85	Sequence 85, Appl
16	296	90.0	295	1	US-08-293-150A-85	Sequence 85, Appl
17	296	90.0	313	1	US-07-791-213D-75	Sequence 75, Appl
18	296	90.0	313	1	US-08-293-150A-75	Sequence 75, Appl
19	296	90.0	343	2	US-08-235-515A-28	Sequence 28, Appl
20	296	90.0	344	1	US-07-972-387-13	Sequence 13, Appl
21	296	90.0	344	1	US-08-431-412-13	Sequence 13, Appl
22	296	90.0	344	1	US-08-057-971-13	Sequence 13, Appl
23	296	90.0	349	1	US-07-972-387-3	Sequence 3, Appl
24	296	90.0	349	1	US-08-431-412-3	Sequence 3, Appl
25	296	90.0	349	1	US-08-057-971-3	Sequence 3, Appl
26	296	90.0	350	1	US-07-791-213D-92	Sequence 92, Appl
27	296	90.0	350	1	US-08-293-150A-92	Sequence 92, Appl
28	296	90.0	441	4	US-09-331-793-28	Sequence 28, Appl
29	296	90.0	624	4	US-09-101-212G-79	Sequence 79, Appl
30	296	90.0	645	4	US-09-101-212G-95	Sequence 95, Appl
31	296	90.0	666	4	US-09-101-212G-97	Sequence 97, Appl
32	295	89.7	343	1	US-07-972-387-5	Sequence 5, Appl
33	295	89.7	343	1	US-08-431-412-5	Sequence 5, Appl
34	295	89.7	343	1	US-08-057-971-5	Sequence 5, Appl
35	294	89.4	240	4	US-09-101-212G-75	Sequence 75, Appl
36	294	89.4	253	4	US-09-101-212G-16	Sequence 16, Appl
37	294	89.4	259	1	US-08-325-243A-2	Sequence 2, Appl
38	294	89.4	261	4	US-09-101-212G-17	Sequence 17, Appl
39	287	87.2	210	1	US-07-791-213D-14	Sequence 14, Appl
40	287	87.2	210	1	US-08-293-150A-14	Sequence 14, Appl
41	287	87.2	313	1	US-07-791-213D-88	Sequence 88, Appl
42	287	87.2	313	1	US-07-972-387-1	Sequence 1, Appl
43	287	87.2	313	1	US-08-431-412-1	Sequence 1, Appl
44	287	87.2	313	1	US-08-057-971-1	Sequence 1, Appl
45	287	87.2	313	1	US-08-293-150A-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-358-160-68
Sequence 68, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

STREET: 419 Seventh Street, N.W. Suite 3000
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

1 SENIOR INVENTOR: 1
2 APPLICANT: LEY, Arthur C. 2
3 APPLICANT: LADNER, Robert C. 3
4 APPLICANT: GUTERMAN, Sonia K. 4
5 APPLICANT: ROBERTS, Bruce L. 5
6 APPLICANT: MARKLAND, William 6
7 APPLICANT: KENT, Rachel B. 7
8 TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ 8

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 8590 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: DNA plasmid
US-08-358-160-70
Alignment Scores:
Pred. No.: 6.24e-37 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-358-160-70 (1-8590)
QY 2 AlaCySaenLeuProIleValaIArgGlyProCySilealaphnePheProArgTTPalaph 21
DB 1212 GCTTGAATCTGCGCATGCTGAGAGTCCATGCTTCTTCTCCAGATGGGCTTTC 1271
QY 22 AspaIaVallysglyLysCySaValleupheProTyrglygLyCySgInglYASnglyASn 41
DB 1272 GACGCTGTAAGGTAAGTGGCTTGTTCCTATCGGTAAGTGTGCAAGGTAAAGGTAAAC 1331
QY 42 LysPheTySerGluLysGluCySaArgGlyTyrcySgIyValPro 56
DB 1332 AAGTTCTACTCTGAGAAAGAGTGAAGAGTACTGTGTGTTCCA 1376

RESULT 4
US-07-791-213D-12
Sequence 12, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
TITLE OF INVENTION: TREATING USING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-12
Alignment Scores:
Pred. No.: 4.69e-35 Length: 198
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-07-791-213D-12 (1-198)
QY 2 AlaCySaenLeuProIleValaIArgGlyProCySilealaphnePheProArgTTPalaph 21
DB 10 GCTGCAATCTCCCATGTCGAGGCGCCCTGCGAGCTTCATCCACTCTGGGCATTT 69
QY 22 AspaIaVallysglyLysCySaValleupheProTyrglygLyCySgInglYASnglyASn 41
DB 70 GATGCTGTCAGAGGGAAGTGGCTCTTCTCCCTACGAGGAGCTGCAAGGCAACAGGAAAC 129
QY 42 LysPheTySerGluLysGluCySaArgGlyTyrcySgIyValPro 56
DB 130 AAGTTCTACTCTGAGAAAGAGTGAAGAGTACTGTGTGTTCCCT 174
RESULT 5
US-08-293-150A-12
Sequence 12, Application US/08293150A

```

: Patent No. 5792629
:
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshimori
: APPLICANT: NOBUHARA, Masahiro
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DONALD, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-NOV-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 198 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-293-150A-12
:
: Alignment Scores:
: Pred. No: 4,69e-35 length: 198
: Score: 296.00 Matches: 51
: Percent Similarity: 92.73% Conservative: 0
: Best Local Similarity: 92.73% Mismatches: 4
: Query Match: 89.97% Indels: 0
: DB: 1 Gaps: 0
:
: US-10-038-722-27 (1-56) x US-08-293-150A-12 (1-198)
:
: Oy 2 AlAcysasnleuProlleValAlaArgjYProCysIleAlaPheProArjTrpAlaPhe 21
: Db 10 GCCGCAATCTCCCATAGTCGGGGGCCCTCCGACAGCTTATCAGACTCTGGGCATT 69
:
: Oy 22 AspaLaValysGlyYsCysValleuPheProTYrgIyGlyYsGlnGlyAsnGlyAsn 41
: Db 70 GATGCTGTCAAGGGGAAGTCGTCTCTTCCCTACGGGGGCTGCCAGGCAAGCGGAC 122
:
: Oy 42 LysPheTySerGluYsGluYsCysArgGluTYrCysGlyValPro 56
: Db 130 AAGTTCTACTCAGAGGAAGAGTCAGAGAGTACTGGGTGTCCT 174
:
: RESULT 6
: US-09-331-793-27
: Sequence 27, Application US/09311793

```

```

Patent No. 6500646
GENERAL INFORMATION:
APPLICANT: KIRIYAMA, Shinichi
APPLICANT: HASEGAWA, Takaehi
TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
FILE REFERENCE: 1110-253P
CURRENT APPLICATION NUMBER: US/09/331,793
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 204
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-331-793-27

Alignment Scores:
Pred. No.: 4,88e-35 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 4 Gaps: 0

US-10-038-722-27 (1-56) x US-09-331-793-27 (1-204)

Qy 2 ALGCAASHLEUPROLEVALRGVLYPROCYSTLEALAPHEPHEPROAARGTTPALAPHE 21
Db 4 GCGTCGAAATCTCCCACTACTCCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCATT 63

Qy 22 ASDALVALYSGLYVYSCYVALLEUPHEPROTYRGYLYGYCYSGINGLYAENGLYASN 41
Db 64 GATGCTGTCAAGGGGAAGTGCCTCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAC 122

Qy 42 LVAPHETYSERGILVYSGINCYAARGGLVYRYCYSGIYVALPRO 56
Db 124 AAGTCTACTACAGAGAAAGAGTGCAGAGAGTACTCGGTGTCCT 168

RESULT 7
US-07-791-213D-15
: Sequence 15, Application US/07791213D
: Patent No. 5409895
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshimori
: APPLICANT: NOBUHARA, Masahiro
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: TITLE OF INVENTION: TREATING USING THE SAME
: NUMBER OF SEQUENCES: 108
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/791,213D
: FILING DATE: 13-NOV-1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M
: REGISTRATION NUMBER: 36,607

```

REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-15

Alignment Scores:
Pred. No.: 5,05e-35 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-15 (1-209)

Qy 2 AlaCysaenleuproilevalarglyprocysillealaphhepProargTtpalaph 21
Db 10 GCTGCAATCTCCCATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCTGGGCATTT 69
Qy 22 AspalavallylglylvscysvalleuphepProtyrglylglycysglinglyAsnGlyasn 41
Db 70 GATGCTGTCAGAGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCGAGGGCAACGGGAAC 129
Qy 42 LysPheTysSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 130 AAGTTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 174

RESULT 8
US-08-293-150A-15.
Sequence 15, Application US/08293150A
Patent No. 5792629

GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-15

Alignment Scores:
Pred. No.: 5,05e-35 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-293-150A-15 (1-209)

Qy 2 AlaCysaenleuproilevalarglyprocysillealaphhepProargTtpalaph 21
Db 10 GCTGCAATCTCCCATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCTGGGCATTT 69
Qy 22 AspalavallylglylvscysvalleuphepProtyrglylglycysglinglyAsnGlyasn 41
Db 70 GATGCTGTCAGAGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCGAGGGCAACGGGAAC 129
Qy 42 LysPheTysSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 130 AAGTTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 174

RESULT 9
US-07-791-213D-11
Sequence 11, Application US/07791213D
Patent No. 5409695

GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-11

Alignment Scores:
Pred. No.: 5.08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-11 (1-210)

QY 2 AlaCysAenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
Db 10 GCCTCAATCTCCCATATGTCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyLysCysValIeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 70 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
Db 130 AAGTTCTACTCAGAGAGAGTGCAGAGAGTACTGGCGGTGCCCT 174

RESULT 10
US-07-972-387-74
; Sequence 74, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanemori, Toshinori
; APPLICANT: No. 5451659hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ. ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..210
; OTHER INFORMATION: /label= sequence
; OTHER INFORMATION: /note= "encodes TN70 polypeptide"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..210
US-07-972-387-74

Alignment Scores:
Pred. No.: 5.08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-972-387-74 (1-210)

QY 2 AlaCysAenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
Db 10 GCCTCAATCTCCCATATGTCGGGGCCCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyLysCysValIeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 70 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
Db 130 AAGTTCTACTCAGAGAGAGTGCAGAGAGTACTGGCGGTGCCCT 174

RESULT 11
US-08-431-742-74
; Sequence 74, Application US/08431412
; Patent No. 5589360
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanemori, Toshinori
; APPLICANT: No. 5589360hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,412
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/972,387
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300

TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: -
LOCATION: 1..210
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "encodes TN70 polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
US-08-431-412-74
Alignment Scores:
Pred. No.: 5,08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-431-412-74 (1-210)
QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCGCGGCCCTGCGAGCCTTCATCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyVbCysValLeuPheProTyrgIyGySgInglYAsnGlYAsn 41
DB 70 GATGCTGCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAA 129
QY 42 LysPheTySerGluIySgIyCysArgIuTyrcYsgIyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGTACTGGGTGTCCCT 174
RESULT 12
US-08-057-971-74
Sequence 74, Application US/08057971
GENERAL INFORMATION:
PATENT No. 5679770
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5679770uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,971
FILING DATE: 06-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.

REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-129P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: -
LOCATION: 1..210
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "encodes TN70 polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
US-08-057-971-74
Alignment Scores:
Pred. No.: 5,08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-057-971-74 (1-210)
QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCGCGGCCCTGCGAGCCTTCATCAGCTCTGGGCATTT 69
QY 22 AspaIaValIySgIyVbCysValLeuPheProTyrgIyGySgInglYAsnGlYAsn 41
DB 70 GATGCTGCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAA 129
QY 42 LysPheTySerGluIySgIyCysArgIuTyrcYsgIyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGTACTGGGTGTCCCT 174
RESULT 13
US-08-293-150A-11
Sequence 11, Application US/08293150A
PATENT No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/791,213D
 FILING DATE: 13-NOV-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 2-306745
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M
 REGISTRATION NUMBER: 36,607
 REFERENCE/DOCKET NUMBER: 029650-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 85:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 27..290
 US-07-791-213D-85

Alignment Scores:
 Pred. No.: 8,14e-35 Length: 295
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 Gaps: 0
 DB: 1

US-10-038-722-27 (1-56) x US-07-791-213D-85 (1-295)
 QY 2 AlaCyAaenLeupPcoIleValArgGlyProCySileAlaPheProArgTrpAlaPhe 21
 Db 99 GCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATTT 158
 QY 22 AspaIaValIySgIyLysCySValIeupheProTyrgIyGlyCySgIyAasnGlyAan 41
 Db 159 GATGCTGCAAGGGGAAGTGCCTCTTCCCTACGCGGGGCTGCCAGGGCAACGGGAAC 218
 QY 42 LysPheTySerGluLysGluCyAArgGluTyrcySgIyValPro 56
 Db 219 AAGTTCTACTCAGAGAGAGAGTGCAGAGATGCTCGGTTCCCT 263

RESULT 16
 US-08-293-150A-85
 ; Sequence 85, Application US/08293150A
 ; Patent No. 5792629
 ; GENERAL INFORMATION:
 ; APPLICANT: MORISHITA, Hideaki
 ; APPLICANT: KANAMORI, Toshinori
 ; APPLICANT: NOBUHARA, Masahiro
 ; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 ; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 ; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 ; TITLE OF INVENTION: TREATING USING THE SAME
 ; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: P. O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/293,150A
 FILING DATE: 19-AUG-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/791,213
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M.
 REGISTRATION NUMBER: 36,607
 REFERENCE/DOCKET NUMBER: 029650-049
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 85:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 27..290
 US-08-293-150A-85

Alignment Scores:
 Pred. No.: 8,14e-35 Length: 295
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 Gaps: 0
 DB: 1

US-10-038-722-27 (1-56) x US-08-293-150A-85 (1-295)
 QY 2 AlaCyAaenLeupPcoIleValArgGlyProCySileAlaPheProArgTrpAlaPhe 21
 Db 99 GCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATTT 158
 QY 22 AspaIaValIySgIyLysCySValIeupheProTyrgIyGlyCySgIyAasnGlyAan 41
 Db 159 GATGCTGCAAGGGGAAGTGCCTCTTCCCTACGCGGGGCTGCCAGGGCAACGGGAAC 218
 QY 42 LysPheTySerGluLysGluCyAArgGluTyrcySgIyValPro 56
 Db 219 AAGTTCTACTCAGAGAGAGAGTGCAGAGATGCTCGGTTCCCT 263

RESULT 17
 US-07-791-213D-75
 ; Sequence 75, Application US/07791213D
 ; Patent No. 5409895
 ; GENERAL INFORMATION:
 ; APPLICANT: MORISHITA, Hideaki
 ; APPLICANT: KANAMORI, Toshinori
 ; APPLICANT: NOBUHARA, Masahiro
 ; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 ; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 ; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 ; TITLE OF INVENTION: TREATING USING THE SAME
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P. O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia

COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 27..303
US-07-791-213D-75

Alignment Scores:
Pred. No.: 8,84e-35 Length: 313
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-75 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 99 GCCTGCAATCTCCCATATCTCCGGGGCCCTGCGAGCTTCATCCAGCTCGGGCATTT 158

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrgIyGlyCysGlnIyAsnIyAsn 41
DB 159 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGGAACGGGAAC 218

QY 42 LysPheTySerGluLysGluCysArgGluTyrcysGlyValPro 56
DB 219 AAGTCTACTCAGAGAGGAGTGACAGAGTACTGCGGTGTCCT 263

RESULT 18
US-08-293-150A-75
Sequence 75, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATHIAS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 27..303
US-08-293-150A-75

Alignment Scores:
Pred. No.: 8,84e-35 Length: 313
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-293-150A-75 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 99 GCCTGCAATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCGGGCATTT 158

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrgIyGlyCysGlnIyAsnIyAsn 41
DB 159 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGGAACGGGAAC 218

QY 42 LysPheTySerGluLysGluCysArgGluTyrcysGlyValPro 56
DB 219 AAGTCTACTCAGAGAGGAGTGACAGAGTACTGCGGTGTCCT 263

RESULT 19
US-08-235-515A-28
Sequence 28, Application US/08235515A
Patent No. 5840518
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshihori
APPLICANT: No. 5840518uhara, Masahiro
TITLE OF INVENTION: DNA FRAGMENT, VECTOR CONTAINING THE DNA
TITLE OF INVENTION: FRAGMENT, TRANSFORMANT TRANSFORMED WITH THE VECTOR AND
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEIN USING THE VECTOR
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747

CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,515A
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-135P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..343
OTHER INFORMATION: /label= polynucleotide
OTHER INFORMATION: /note= "j-x1-y-z (AN68), insert in plasmid pM710,
FEATURE: Figure 11"
NAME/KEY: sig_peptide
LOCATION: 27..89
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 90..329
FEATURE:
NAME/KEY: CDS
LOCATION: 27..329
US-08-235-515A-28
Alignment Scores:
Pred. No.: 1e-34 Length: 343
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB: 2
US-10-038-722-27 (1-56) x US-08-235-515A-28 (1-343)
QY 2 AlaCysanleuprollevalarglyProCysillealapheProargtrpAlaphe 21
Db 129 GCCTGTATCTACCAATATGTCGGGGCCCCCTGCCAGCCTTCATCCAGCTCTGGGCAATT 188
QY 22 AspaIaVallysglyLysCysValleupheProtyrglyGlyGlnGlyAsnGlyAsn 41
Db 189 GATCCTGTCAAGAGGAGAGTGGCTCTCTCCCTACGGGGGAGCTGCCAGGGCAACGGGAAAC 248
QY 42 LysheTySerGlyLysGlyCysArgGlyLysGlyValPro 56
Db 249 AAGTTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGCCCT 293
RESULT 20
US-07-972-387-13
; Sequence 13, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori

APPLICANT: No. 5451659uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
TITLE OF INVENTION: Producing the Same
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,387
FILING DATE: 19921105
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: J55055 (pM576B)
FEATURE:
NAME/KEY: -
LOCATION: 1..344
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "as in Figure 31"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 44..106
OTHER INFORMATION: /standard_name= "pho A signal
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 107..310
OTHER INFORMATION: /standard_name= "polypeptide
OTHER INFORMATION: Q19K-AN"
FEATURE:
NAME/KEY: CDS
LOCATION: 44..310
US-07-972-387-13
Alignment Scores:
Pred. No.: 1.01e-34 Length: 344
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB: 1
US-10-038-722-27 (1-56) x US-07-972-387-13 (1-344)
QY 2 AlaCysanleuprollevalarglyProCysillealapheProargtrpAlaphe 21
Db 110 GCCTGTATCTACCAATATGTCGGGGCCCCCTGCCAGCCTTCATCCAGCTCTGGGCAATT 169

QY 22 Aspa1aVal1ySG1yLysCyVal1euPheProTyrg1yG1yCySG1ng1yAasn1yAasn 41
| | | | |
DB 170 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 229
| | | | |
QY 42 LysPheTySerG1uLysG1uCyAarg1uTyrcySG1yVal1pro 56
| | | | |
DB 230 AAGTCTACTCAGAGAAGAGTGCAGAGTACTCGGTGTCCT 274
| | | | |
RESULT 21
US-08-431-412-13
; Sequence 13, Application US/08431412
; Patent No. 5589360
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5589360uhara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; TITLE OF INVENTION: Producing the Same
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,412
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/972,387
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: JES055 (pms76b)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..344
; OTHER INFORMATION: /label= sequence
; OTHER INFORMATION: /note= "as in Figure 31"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 44..106
; OTHER INFORMATION: /standard_name= "pho A signal
; OTHER INFORMATION: sequence=""
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 107..310
; OTHER INFORMATION: /standard_name= "polypeptide

; OTHER INFORMATION: Q19K-AN"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..310
US-08-431-412-13
Alignment Scores:
Pred. No.: 1,01e-34 Length: 344
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-431-412-13 (1-344)
QY 2 AlaCysAsn1euProl1eVal1Arg1yProCyVal1eAlaPheProArg1Phe 21
| | | | |
DB 110 GCCTGTATCTACCAATATGTCGGGGCCCTGCCGAGCTTCATCAAGCTCTGGGCATTT 169
| | | | |
QY 22 Aspa1aVal1ySG1yLysCyVal1euPheProTyrg1yG1yCySG1ng1yAasn1yAasn 41
| | | | |
DB 170 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 229
| | | | |
QY 42 LysPheTySerG1uLysG1uCyAarg1uTyrcySG1yVal1pro 56
| | | | |
DB 230 AAGTCTACTCAGAGAAGAGTGCAGAGTACTCGGTGTCCT 274
| | | | |
RESULT 22
US-08-057-971-13
; Sequence 13, Application US/08057971
; Patent No. 5679770
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5679770uhara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; TITLE OF INVENTION: Producing the Same
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/057,971
; FILING DATE: 06-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-129P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:

```

; ORGANISM: Escherichia coli
; STRAIN: JES505 (PM576B)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..344
; OTHER INFORMATION: /label= sequence
; OTHER INFORMATION: /note= "as in Figure 31"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 44..106
; OTHER INFORMATION: /standard_name= "pho A signal"
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 107..310
; OTHER INFORMATION: /standard_name= "polypeptide"
; OTHER INFORMATION: Q19K-AN"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..310
; US-08-057-971-13

Alignment Scores:
Pred. No.: 1.03e-34 Length: 344
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-057-971-13 (1-344)
Qy 2 AlaCyAsenLeuProIleValArgIleProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 110 GCCTGTAATCTACCAATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCTGGGCATTT 169
Qy 22 AspaValAllySGlyVlySCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 170 GATGCTGTCAAGGGGAAAGTGCCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAAC 229
Qy 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 230 AAGTCTACTCAGAGAGAGAGTGCAGAGTACTCGGTGTCCT 274

RESULT 23
; Sequence 3, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshihiko
; APPLICANT: No. 5451659uhara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1900
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: JES505 (PM576)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..349
; OTHER INFORMATION: /label= sequence
; OTHER INFORMATION: /note= "as in Figure 16"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 44..106
; OTHER INFORMATION: /standard_name= "pho A signal"
; OTHER INFORMATION: peptide"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 107..316
; OTHER INFORMATION: /product= "polypeptide Q19K"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..316
; US-07-972-387-3

Alignment Scores:
Pred. No.: 1.03e-34 Length: 349
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-972-387-3 (1-349)
Qy 2 AlaCyAsenLeuProIleValArgIleProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 116 GCCTGCAATCTCCCATATGTCGGGGCCCCCTGCCAGCCTTCATCAAGCTCTGGGCATTT 175
Qy 22 AspaValAllySGlyVlySCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 176 GATGCTGTCAAGGGGAAAGTGCCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAAC 235
Qy 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 236 AAGTCTACTCAGAGAGAGTGCAGAGTACTCGGTGTCCT 280

RESULT 24
; Sequence 3, Application US/08431412
; Patent No. 5589360
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshihiko
; APPLICANT: No. 5589360uhara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
```


STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,412
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/972,387
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: JES505 (pm576)
FEATURE:
NAME/KEY: -
LOCATION: 1..349
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "as in figure 16"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 44..106
OTHER INFORMATION: /standard_name= "pho A signal"
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 107..316
OTHER INFORMATION: /product= "polypeptide Q19K"
FEATURE:
NAME/KEY: CDS
LOCATION: 44..316
US-08-431-412-3
Alignment Scores:
Pred. No.: 1.03e-34 Length: 349
Score: 296.00 Matches: 51
Percent Similarity: 92.738 Conservative: 0
Best Local Similarity: 92.738 Mismatches: 4
Query Match: 89.974 Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-431-412-3 (1-349)
QY 2 AAlaCyAsnLeuProIleValArgIleProCysIleAlaPheProArgTyrAlaPhe 21
DB 116 GCCTGCAATCTCCCATAGTCCGGGCCCCCTGCGGAGCTTCATCAAGCTCTGGGCAATT 175
QY 22 AappAlaValIleGlyGlyGlyGlyValIleuPheProTyrGlyGlyCysGlnIleGlyAsn 41
DB 176 GATGCTGTCAAGGGGAAAGTGCCTCTTCCCTACGGGGGCTGCGAGGCAACGGGAAC 235

QY 42 LysPheTyrSerGluTyrGlyCysArgGluTyrCysGlyValPro 56
DB 236 AAGTTCTACTCAGAGAGAGAGTGCAGAGATGAGTGCCTGCTCCCT 280
RESULT 25
US-08-057-971-3
Sequence 3, Application US/08057971
Patent No. 5679770
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5679770uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,971
FILING DATE: 06-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-129P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: JES505 (pm576)
FEATURE:
NAME/KEY: -
LOCATION: 1..349
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "as in figure 16"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 44..106
OTHER INFORMATION: /standard_name= "pho A signal"
OTHER INFORMATION: peptide
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 107..316
OTHER INFORMATION: /product= "polypeptide Q19K"
FEATURE:
NAME/KEY: CDS
LOCATION: 44..316
US-08-057-971-3
Alignment Scores:
Pred. No.: 1.03e-34 Length: 349
Score: 296.00 Matches: 51

Percent Similarity: 92.73%
 Best Local Similarity: 92.73%
 Query Match: 89.97%
 DB: 1
 Conservative: 0
 Mismatches: 4
 Indels: 0
 Gaps: 0

US-10-038-722-27 (1-56) x US-08-057-971-3 (1-349)

Oy	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe	21
Db	116	GCCTCCATCTCCCATAGTCGGGGCCCCCTCCGAGCCTTCATCAAGCTCGGGCATTT	175
Oy	22	AspAlaValIlyGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn	41
Db	176	GATGCTGCAAGGGAGAGTCGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC	235
Oy	42	LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
Db	236	AAGTTCTACTCAGAGAGAGAGTACGAGAGTACTGGGTTGTCCT	280

Search completed: February 23, 2005, 06:04:39
 Job time : 140 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 01:42:48 ; Search time 74 Seconds

(without alignment)
292.684 Million cell updates/sec

Title: US-10-038-722-27

Sequence: 1 EACNLPYRGPICIAFFPRWA.....QGNKRYSEKREYCGVP 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	56	AAR99168	Aar99168 Genetical
2	329	100.0	56	AdF42070	AdF42070 Albinism f
3	329	100.0	56	AdF71969	AdF71969 Kallikrein
4	329	100.0	56	AdR90015	AdR90015 DX-890 (a
5	329	100.0	141	AAR99215	Aar99215 Modified
6	329	100.0	141	ABR84583	AbR84583 P pastor
7	329	100.0	141	ABR84585	AbR84585 Fusion se
8	329	100.0	655	AdF42042	AdF42042 N-termina
9	329	100.0	655	AdF42044	AdF42044 C-termina
10	329	100.0	655	AdR90036	AdR90036 C-termina
11	329	100.0	655	AdR90034	AdR90034 N-termina
12	329	100.0	694	AdF42054	AdF42054 Plasmid p
13	329	100.0	694	AdR90046	AdR90046 PDB2300X2
14	329	100.0	728	AdF42058	AdF42058 Albumin f
15	329	100.0	728	AdR90050	AdR90050 Mature PD
16	329	100.0	729	AdF42029	AdF42029 DFI-14-(G
17	329	100.0	729	AdR90021	AdR90021 Mature DP
18	329	100.0	752	AdF42057	AdF42057 Plasmid p
19	329	100.0	752	AdR90049	AdR90049 PDB2300X3
20	329	100.0	753	AdF42028	AdF42028 DFI-14-(G
21	329	100.0	753	AdR90020	AdR90020 DFI-14-(G
22	324	98.5	56	AdR99167	AdR99167 Genetical
23	324	98.5	56	AdF71967	AdF71967 Kallikrei
24	324	98.5	56	AdF71968	AdF71968 Kallikrei
25	324	98.5	141	AAR99214	Aar99214 Modified

26	307	93.3	66	2	AAR61165
27	301	91.5	66	2	AAR61156
28	300	91.2	66	2	AAR61158
29	299	90.9	66	2	AAR61157
30	296	90.0	57	3	ABR14179
31	296	90.0	58	2	AAR78555
32	296	90.0	58	2	AAR81927
33	296	90.0	58	2	AAR91666
34	296	90.0	58	2	AAW64116
35	296	90.0	58	2	AAW92863
36	296	90.0	58	7	AdF42000
37	296	90.0	58	8	AdF71951
38	296	90.0	58	8	AdR89983
39	296	90.0	66	2	AAR61162
40	296	90.0	68	2	AAR65478
41	296	90.0	68	2	AAR92232
42	296	90.0	68	2	AAW25930
43	296	90.0	68	2	AAW69521
44	296	90.0	69	2	AAR99698
45	296	90.0	70	2	AAR65481

ALIGNMENTS

RESULT 1
AAR99168 standard; protein; 56 AA.

12-FEB-1997 (first entry)

Genetically engineered aprotinin-like Kunitz domain (EPI-HNE-4).

Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.

OS Synthetic.

PN WO9620278-A2.

PD 04-JUL-1996.

PF 15-DEC-1995; 95WO-US016349.

PR 16-DEC-1994; 94US-00358160.

(PROT-) PROTEIN ENG CORP.

WPI, 1996-321851/32.

WPI, 1996-321851/32.

New engineered inhibitors of human neutrophil elastase - contg. aprotinin
-like Kunitz domain for treating, e.g. cystic fibrosis or other
respiratory disorders.

Claim 1; Page 49; 105pp; English.

Genetically engineered human derived Kunitz domains can be used to
inhibit human neutrophil elastase, an enzyme involved in the elimination
of pathogens and the restructuring of connective tissue. In cases of
reduction of the circulating alpha-1-protease inhibitor (API or alpha1
antitrypsin), or the inactivation of API by oxidation (smokers
emphysema), extensive destruction of the lung tissue may result from
uncontrolled elastolytic activity of human neutrophil elastase. Other
respiratory disorders such as cystic fibrosis are thought to be caused by
human neutrophil elastase release by neutrophils. The genetically
engineered human derived Kunitz domains can be used to treat such
respiratory disorders. See AAR99146-R99211

XX
SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 2

ADF42070
ID ADF42070 standard; peptide; 56 AA.

XX ADF42070;

DT 12-FEB-2004 (first entry)

XX Albumin fusion protein-related DX-890 peptide.

DE albumin fusion; Kunitz domain; cytostatic; haemostatic;

XX hereditary angioedema; cancer; bleeding; gene therapy; DX-890.

OS Unidentified.

PN WO2003066824-A2.

PD 14-AUG-2003.

PF 07-FEB-2003; 2003WO-US003616.

PR 07-FEB-2002; 2002US-0355547P.

XX (AVERT) AVENTIS BEHRING GMBH.

PA (AVERT) AVENTIS BEHRING LLC.

PA (DELTA) DELTA BIOTECHNOLOGY LTD.

PA (DVAX-) DVAX CORP.

PI Hauser H, Welmer T, Romberg V, Kee SM, Sleep D, Ladner RC;

PI Ley AC;

DR WPI; 2003-731497/69.

XX Example 7; SEQ ID NO 20; 110pp; English.

CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related DX-890 peptide of
CC the invention.

SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 7; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 3

ADF71969
ID ADF71969 standard; protein; 56 AA.

XX ADF71969;

DT 11-MAR-2004 (first entry)

XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:49.

DE ischaemia; vasotrophic; kallikrein inhibitor; blood loss;

XX systemic inflammatory response.

OS Homo sapiens.

PN WO2003103475-A2.

PD 18-DEC-2003.

PF 06-JUN-2003; 2003WO-US017665.

PR 07-JUN-2002; 2002US-0387239P.

PR 28-AUG-2002; 2002US-0407003P.

PA (DVAX-) DVAX CORP.

PI Ladner RC, Ley AC, Hirani S, Williams A;

PI WPI; 2004-062190/06.

PT Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.

PS Disclosure; SEQ ID NO 49; 46pp; English.

CC The present invention describes a method (M1) for preventing or reducing
CC ischemia in a patient. M1 involves administering to the patient a
CC composition comprising a polypeptide (I) having an amino acid sequence of
CC ADF71969 and inhibiting kallikrein. (I) has vasotrophic activity, and can
CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
CC reducing ischemia in a patient such as perioperative blood loss due to a
CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
CC is also useful for preventing or reducing the onset of systemic
CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (I) to a patient. The present sequence is
CC used in the exemplification of the present invention.

SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 4

ADR90015
ID ADR90015 standard; peptide; 56 AA.

XX ADR90015;

DT 18-NOV-2004 (first entry)

DE DX-890 (an inhibitor of human neutrophil elastase) kunitz domain peptide.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;

KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostatic; haemostatic.

OS Unidentified.
XX
XX US2004171794-A1.
XX
PD 02-SEP-2004.
XX
XX
XX 07-FEB-2003; 2003US-00361997.
XX
PR 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
PI Lader RC, Ley AC;
XX
XX WPI; 2004-625120/60.
DR
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 2; SEQ ID NO 40; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated Dp1-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytostatic and haemostatic agent. The present sequence is a DX-890 (an
CC inhibitor of human neutrophil elastase) kunitz domain peptide. This
CC sequence is used in the exemplification of the invention.
XX
XX Sequence 56 AA;
SQ

Query Match 100.0%; Score 329; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGPCIAFPFPAFDVAVKGCYLFPYGGCCGNGNKFYSKREYCGVP 56
DB 1 EACNLPYRGPCIAFPFPAFDVAVKGCYLFPYGGCCGNGNKFYSKREYCGVP 56

RESULT 5
AAR9215
ID AAR9215 standard; protein; 141 AA.
XX
XX AAR9215;
XX
XX 14-FEB-1997 (first entry)
XX
XX Modified Kunitz domain EPI-HNE-4.
XX
XX Apocitin; Kunitz domain; human neutrophil elastase; hNE;
XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
XX alpha1 antitrypsin; respiratory disorder; cystic fibrosis;
XX smokeless emphysema.
XX
XX Synthetic.
XX
XX WO9620278-A2.
XX
XX 04-JUL-1996.
XX
XX 15-DEC-1995; 95WO-US016349.
XX
XX 16-DEC-1994; 94US-00358160.
XX
XX (PROT-) PROTEIN ENG CORP.
XX
XX Ley AC, Lader RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1996-321851/32.
XX
XX

DR N-PSDB; AAT35168.
XX
XX New engineered inhibitors of human neutrophil elastase - contg. apocitin
PT -like kunitz domain for treating, e.g. cystic fibrosis or other
XX respiratory disorders.
XX
XX Claim 1; Page 68-75; 105pp; English.
XX
XX Genetically engineered human derived kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived kunitz domains can be used to treat such
CC respiratory disorders. See AAR9146-899211. Fusion genes were used in the
CC production of the kunitz domain derivatives. Protein expression cassettes
CC are then cloned into the plasmid pHR-D2 using BstBI and EcoRI
CC restriction sites. The cloned sequence is under the transcriptional
CC control of Pichia pastoris axi gene promoter and regulatory sequences
CC and downstream polyadenylation and transcription termination sequences.
CC Transformed strains of P. pastoris were used to express the various EPI-
CC HNE proteins derived from the BPI and ITI-D2 kunitz domains. This
CC sequence is a modified kunitz domain (EPI-HNE-4) which was expressed from
CC a pHR-D2 plasmid construct
XX
XX Sequence 141 AA;
SQ

Query Match 100.0%; Score 329; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGPCIAFPFPAFDVAVKGCYLFPYGGCCGNGNKFYSKREYCGVP 56
DB 86 EACNLPYRGPCIAFPFPAFDVAVKGCYLFPYGGCCGNGNKFYSKREYCGVP 141

RESULT 6
ABR84583
ID ABR84583 standard; protein; 141 AA.
XX
XX ABR84583;
XX
XX 04-DEC-2003 (first entry)
XX
XX P pastoris prepro-EPI-HNE-4 mutated protein.
XX
XX EPI-HNE-4; EPI-HNE; alpha mating factor prepropeptide; mutant; mutagenic;
XX mutein.
XX
XX Pichia pastoris.
XX
XX Synthetic.
XX
XX WO2003062431-A2.
XX
XX 31-JUL-2003.
XX
XX 23-JAN-2003; 2003WO-EP001212.
XX
XX 23-JAN-2002; 2002EP-00290166.
XX
XX (DEBI-) DEBIOPHARM SA.
XX
XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;
XX WPI; 2003-598755/56.
XX
XX N-PSDB; ACP04569.
XX
XX New fused gene constructs and expression vectors, useful for transforming
PT microorganisms (particularly the yeast Pichia pastoris) for use in

PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly
PT processed form.

XX Example 2; Fig 1B; 27pp; English.

CC The present invention relates to a fused gene construct, which comprises
CC a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n+9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a mutated version
CC of the *Pichia pastoris* EPI-hNE-4 protein used in the exemplification of
CC the invention

XX Sequence 141 AA;

Query Match 100.0%; Score 329; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFPFPRMADAVKGCVLFPYGGCGGNGKFKYSEKCREYCGVP 56
ID ABR84585
ABR84585 standard; protein; 141 AA.

XX ABR84585;

XX 04-DEC-2003 (first entry)

XX Fusion sequence of alpha mating factor and EPI-hNE-4.

XX EPI-hNE-4; EPI-hNE; alpha mating factor prepeptide; fusion protein;
XX mutagenic.

XX *Saccharomyces cerevisiae*.

XX *Pichia pastoris*.

XX WO2003062431-A2.

XX 31-JUL-2003.

XX 23-JAN-2003; 2003WO-EP001212.

XX 23-JAN-2002; 2002EP-00290166.

XX (DEBI-) DEBIOPHARM SA.

XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;

XX WPI; 2003-598755/56.

XX N-PSDB; ACF04571.

XX New fused gene constructs and expression vectors, useful for transforming
PT microorganisms (particularly the yeast *Pichia pastoris*) for use in
PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly
PT processed form.

XX Claim 4; Fig 10; 27pp; English.

XX The present invention relates to a fused gene construct, which comprises

CC a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n+9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a fusion protein
CC containing the *S. cerevisiae* alpha mating factor prepeptide and the
CC *Pichia pastoris* EPI-hNE-4 protein used in the exemplification of the
CC invention

XX Sequence 141 AA;

Query Match 100.0%; Score 329; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFPFPRMADAVKGCVLFPYGGCGGNGKFKYSEKCREYCGVP 56
ID ADF42042
ADF42042 standard; protein; 655 AA.

XX ADF42042;

XX 12-FEB-2004 (first entry)

XX N-terminal DX-890-(GGG)4GG-albumin fusion protein.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;

XX hereditary angioedema; cancer; bleeding; gene therapy;

XX N-terminal DX-890-(GGG)4GG-albumin fusion.

XX Synthetic.

XX Unidentified.

XX WO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVENT) AVENTIS BEHRING GMBH.

XX (AVENT) AVENTIS BEHRING LLC.

XX (DELZ) DELTA BIOTECHNOLOGY LTD.

XX (DVAX-) DVAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

XX Ley AC;

XX WPI; 2003-731497/69.

XX N-PSDB; ADF42041.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX Example 23; Page 75; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its


```

ADR90034
ID ADR90034 standard; protein; 655 AA.
XX
AC ADR90034;
XX
DT 18-NOV-2004 (first entry)
XX
DE N-terminal DX-890-(GGG)4 GG-albumin fusion protein.
XX
KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
hereditary angioedema; cancer; chronic obstructive pulmonary disease;
asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
cystostatic; haemostatic; chimeric; DX-890; human albumin; HA; human.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
XX
PN US2004171794-A1.
XX
PD 02-SEP-2004.
XX
PF 07-FEB-2003; 2003US-00361997.
XX
PR 07-FEB-2003; 2003US-00361997.
XX
PA (LADN/) LADNER R. C.
PA (LEYA/) LEY A. C.
XX
PI Ladner RC, Ley AC;
XX
DR WPI; 2004-625120/60.
DR N-PSDB; ADR90033.
XX
PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
for the treatment of e.g. cystic fibrosis and related disease.
XX
PS Example 8; SEQ ID NO 59; 123bp; English.
XX
CC The invention relates to proteins comprising kunitz domain peptide,
designated DPI-14 for inhibiting human neutrophil elastase, fused to
albumin. The invention is useful for treating cystic fibrosis and related
diseases, hereditary angioedema, cancer and related diseases including
chronic obstructive pulmonary disease, asthma, bronchitis, acute
respiratory syndrome, pneumonia and bleeding. The invention acts as a
cystostatic and haemostatic agent. The present sequence is a N-terminal DX
-890-(GGG)4 GG-albumin fusion protein. This fusion protein contains DX-
890 cDNA encoding protein, GS linker region and human albumin (HA)
encoding protein. This sequence is used in the exemplification of the
invention.
XX
SQ Sequence 655 AA;

Query Match          100.0%; Score 329; DB 8; Length 655;
Best Local Similarity 100.0%; Pred. No. 2,1e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVRGPCIAPFPRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
DB 1 EACNLPYVRGPCIAPFPRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56

RESULT 12
ADR42054
ID ADR42054 standard; protein; 694 AA.
XX
AC ADR42054;
XX
DT 12-FEB-2004 (first entry)
XX
DE Plasmid pDB2300X2 NotI modified expression cassette protein.
XX
KW albumin fusion; Kunitz domain; cystostatic; haemostatic;

```

```

KW hereditary angioedema; cancer; bleeding; gene therapy;
KW plasmid pDB2300X2 NotI expression cassette; DX-890.
XX
OS Synthetic.
OS Unidentified.
XX
PN WO2003066824-A2.
XX
PD 14-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003616.
XX
PR 07-FEB-2002; 2002US-0355547P.
XX
PA (AVET ) AVENTIS BEHRING GMBH.
PA (AVET ) AVENTIS BEHRING LLC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
XX
PI Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
XX
DR WPI; 2003-731497/69.
DR N-PSDB; ADR42053.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
useful for preparing a composition for treating a patient with hereditary
angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
PS Example 23; Page 85-89; 110bp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
Kunitz domain peptide or its fragment or variant and an albumin or its
fragment or variant. The fusion protein of the invention demonstrates
cystostatic and haemostatic activities and may be useful for preparing a
composition for treating a patient with hereditary angioedema, an
angioedema-related disease, cancer, a cancer-related disease or a
bleeding disorder, as well as during gene therapy procedures. The current
sequence is that of the albumin fusion protein-related plasmid pDB2300X2
modified NotI expression cassette protein of the invention which has N-
terminal DX-890 and C-terminal linker ready for a second DX-890 sequence.
XX
SQ Sequence 694 AA;

Query Match          100.0%; Score 329; DB 7; Length 694;
Best Local Similarity 100.0%; Pred. No. 2,2e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVRGPCIAPFPRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
DB 25 EACNLPYVRGPCIAPFPRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 80

RESULT 13
ADR90046
ID ADR90046 standard; protein; 694 AA.
XX
AC ADR90046;
XX
DT 18-NOV-2004 (first entry)
XX
DE pDB2300X2-2XGS linker fusion protein.
XX
KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
hereditary angioedema; cancer; chronic obstructive pulmonary disease;
asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
cystostatic; haemostatic; chimeric; human; rHA synthase gene;
human albumin; HA.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
XX

```

```

FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal_peptide
FT Region 25..694
FT Region /note= "Mature pDB2300X2-2xGS linker fusion protein"
FT Region 25..80
FT Region /note= "DX-890 protein"
FT Region 81..94
FT Region /note= "GS-linker region"
FT Region 95..679
FT Region /note= "rHA protein"
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
XX Ladhner RC, Ley AC;
XX
XX MPI: 2004-625120/60.
XX N-PSDB; ADR90045.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 18; SEQ ID NO 71; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytosolic and haemostatic agent. The present sequence is a pDB2300X2-
XX 2xGS linker fusion protein. This chimeric protein contains DX-890 protein
XX at its N-terminal end, rHA synthase gene encoding protein and linkers at
XX its C-terminal end. This sequence is used in the exemplification of the
XX invention.
XX
XX SQ Sequence 694 AA;
XX
XX Query Match 100.0%; Score 329; DB 8; Length 694;
XX Best Local Similarity 100.0%; Pred. No. 2,2e-33;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 EACNLPYRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGKPFYSEKREYCGVP 56
XX |||||
XX DB 25 EACNLPYRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGKPFYSEKREYCGVP 80
XX |||||
XX
XX RESULT 14
XX ADF42058
XX ID ADF42058 standard; protein; 728 AA.
XX
XX AC ADF42058;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Albumin fusion-related DX-890. (GGS) 4GG. HA. (GGS) 4GG. DX-890 protein.
XX
XX KW albumin fusion; Kunitz domain; cytosolic; haemostatic;
XX hereditary angioedema; cancer; bleeding; gene therapy; (GGS) 4GG; DX-890;
XX HA.
XX
XX OS Synthetic.
XX Unidentified.
XX
```

```

PN WO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET ) AVENTIS BEHRING GMBH.
XX (AVET ) AVENTIS BEHRING LLC.
XX (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladhner RC;
XX Ley AC;
XX
XX MPI: 2003-731497/69.
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
XX useful for preparing a composition for treating a patient with hereditary
XX angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX Example 23; Page 94-95; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
XX Kunitz domain peptide or its fragment or variant and an albumin or its
XX fragment or variant. The fusion protein of the invention demonstrates
XX cytosolic and haemostatic activities and may be useful for preparing a
XX composition for treating a patient with hereditary angioedema, an
XX angioedema-related disease, cancer, a cancer-related disease or a
XX bleeding disorder, as well as during gene therapy procedures. The current
XX sequence is that of the albumin fusion protein-related DX-
XX 890. (GGS) 4GG. HA. (GGS) 4GG. DX-890 protein of the invention.
XX
XX SQ Sequence 728 AA;
XX
XX Query Match 100.0%; Score 329; DB 7; Length 728;
XX Best Local Similarity 100.0%; Pred. No. 2,3e-33;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 EACNLPYRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGKPFYSEKREYCGVP 56
XX |||||
XX DB 1 EACNLPYRGPCIAFPFPRWAFDAVKGKCVLPFYGGCGGNGKPFYSEKREYCGVP 56
XX |||||
XX
XX RESULT 15
XX ADR90050
XX ID ADR90050 standard; protein; 728 AA.
XX
XX AC ADR90050;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Mature pDB2300X3-2xDX-890 fusion protein.
XX
XX KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cytosolic; haemostatic; chimeric; human; rHA synthase gene;
XX human albumin; HA; DX-890.
XX
XX OS Homo sapiens.
XX Chimeric.
XX Unidentified.
XX
XX PN US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
```

PA (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX
 PI Ladner RC, Ley AC;
 XX
 DR WPI; 2004-625120/60.
 DR N-PSDB; ADR90048.
 XX
 PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX
 PS Example 19; SEQ ID NO 75; 123pp; English.
 XX
 CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytoskeletal and haemostatic agent. The present sequence is a mature
 CC PDB3100X3-2XDX-890 fusion protein. This chimeric protein contains two DX-
 CC 890 proteins, rHA synthase gene encoding protein and the linkers. This
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 728 AA;
 XX
 Query Match 100.0%; Score 329; DB 8; Length 728;
 Best Local Similarity 100.0%; Pred. No. 2.3e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
 DB 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
 XX
 RESULT 16
 ADF42029
 ID ADF42029 standard; protein; 729 AA.
 XX
 AC ADF42029;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion mature protein.
 XX
 KM albumin fusion; kunitz domain; cytoskeletal; haemostatic;
 KM hereditary angioedema; cancer; bleeding; gene therapy; plasmid PDB3101X;
 KM DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion; mature.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN WO2003066824-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003WO-US003616.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 XX
 PA (AVENT) AVENTIS BEHRING GMBH.
 PA (AVENT) AVENTIS BEHRING LLC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (DYAX-) DYAX CORP.
 XX
 PI Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC,
 PI Ley AC;
 XX
 DR WPI; 2003-731497/69.
 XX
 PT Albumin fusion protein comprising a kunitz domain peptide and an albumin,
 PT useful for preparing a composition for treating a patient with hereditary
 PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX
 PS Example 22; Page 68-69; 110pp; English.
 XX
 CC The invention relates to a novel albumin fusion protein comprising a
 CC kunitz domain peptide or its fragment or variant and an albumin or its
 CC fragment or variant. The fusion protein of the invention demonstrates
 CC cytoskeletal and haemostatic activities and may be useful for preparing a
 CC composition for treating a patient with hereditary angioedema, an
 CC angioedema-related disease, cancer, a cancer-related disease or a
 CC bleeding disorder, as well as during gene therapy procedures. The current
 CC sequence is that of the plasmid PDB3101X-derived DPI-14- (GGS) 4GG-rHA-
 CC (GGS) 4GG-DX-890 fusion mature protein of the invention.
 XX
 SQ Sequence 729 AA;
 XX
 Query Match 100.0%; Score 329; DB 7; Length 729;
 Best Local Similarity 100.0%; Pred. No. 2.3e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
 DB 674 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 729
 XX
 RESULT 17
 ADR90021
 ID ADR90021 standard; protein; 729 AA.
 XX
 AC ADR90021;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Mature DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein.
 XX
 KM kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 KM hereditary angioedema; cancer; chronic obstructive pulmonary disease;
 KM asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KM cytoskeletal; haemostatic; human; rHA synthase gene; human albumin; HA;
 KM DPI-14; DX-890; chimeric.
 XX
 OS Homo sapiens.
 OS Chimeric.
 OS Unidentified.
 XX
 PN US2004171794-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 07-FEB-2003; 2003US-00361997.
 XX
 PR 07-FEB-2003; 2003US-00361997.
 XX
 PA (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX
 PI Ladner RC, Ley AC;
 XX
 DR WPI; 2004-625120/60.
 DR N-PSDB; ADR90019.
 XX
 PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX
 PS Example 22; SEQ ID NO 46; 123pp; English.
 XX
 CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytoskeletal and haemostatic agent. The present sequence is a mature DPI-14
 CC - (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein. This fusion protein

CC contains DPI-14 cDNA encoding protein, GS linker region, rHA (human
CC albumin) synthase gene encoding protein and DX-890 encoding protein. This
CC sequence is used in the exemplification of the invention.
XX
SQ Sequence 729 AA;

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2,3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 674 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 729

RESULT 18
ADP42057
ID ADP42057 standard; protein; 752 AA.
XX
AC ADP42057;
XX

DT 12-FEB-2004 (first entry)

XX Plasmid PDB2300X3 NotI modified expression cassette protein - 2X DX-890.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
KM hereditary angioedema; cancer; bleeding; gene therapy;
KM plasmid PDB2300X3 NotI expression cassette; DX-890..

XX Synthetic.
OS Unidentified.

XX MO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVET) AVENTIS BEHRING GMBH.

XX (AVET) AVENTIS BEHRING LLC.

XX (DELZ) DELTA BIOTECHNOLOGY LTD.

XX (DYAX-) DYAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;

XX WPI; 2003-731497/69.

XX N-PSDB; ADP42056.

XX Example 23; Page 91-94; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a

XX Kunitz domain peptide or its fragment or variant and an albumin or its

XX fragment or variant. The fusion protein of the invention demonstrates

XX cytostatic and haemostatic activities and may be useful for preparing a

XX composition for treating a patient with hereditary angioedema, an

XX angioedema-related disease, cancer, a cancer-related disease or a

XX bleeding disorder, as well as during gene therapy procedures. The current

XX sequence is that of the albumin fusion protein-related plasmid PDB2300X3

XX modified NotI expression cassette protein of the invention which has 2 DX

XX -890 sequences.

XX Sequence 752 AA;

Qy 1 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 25 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 7; Length 752;
Best Local Similarity 100.0%; Pred. No. 2,4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
Db 25 EACNLPYVRGPCIAFFPRMAFDAYKGCVLFPYGGCCGNGNKFYSEKREYCGVP 80

RESULT 19
ADR90049
ID ADR90049 standard; protein; 752 AA.
XX
AC ADR90049;
XX
DT 18-NOV-2004 (first entry)

XX Plasmid PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KM hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KM asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KM cytostatic; haemostatic; chimeric; human; rHA synthase gene;
KM human albumin; HA; DX-890.

XX Homo sapiens.
OS Chimeric.
OS Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX
SQ Sequence 752 AA;

Query Match 100.0%; Score 329; DB 8; Length 752;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 25 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 80

RESULT 20
ADFA42028
ID ADFA42028 standard; protein; 753 AA.

AC ADFA42028;

DT 12-FEB-2004 (first entry)

DE DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion precursor protein.

KW albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy; plasmid PDB2301X;
KW DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion; precursor.

OS Synthetic.
OS Unidentified.

PN WO2003066824-A2.

PD 14-AUG-2003.

PF 07-FEB-2003; 2003WO-US003616.

PR 07-FEB-2002; 2002US-0355547P.

PA (AVET) AVENTIS BEHRING GMBH.

PA (AVET) AVENTIS BEHRING LLC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (DYAX-) DYAX CORP.

PI Hauser H, Weimer T, Romberg V, Kee SM, sleep D, Ladner RC;

PI Ley AC;

XX MPI: 2003-731497/69.

DR N-PSDB; ADFA42068.

PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

PS Example 22; Page 68; 110pp; English.

CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the plasmid PDB2301X-derived DPI-14- (GGS) 4GG-rHA-
CC (GGS) 4GG-DX-890 fusion precursor protein of the invention.

XX Sequence 753 AA;

Query Match 100.0%; Score 329; DB 7; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 698 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 753

RESULT 21
ADR90020
ID ADR90020 standard; protein; 753 AA.

AC ADR90020;

DT 18-NOV-2004 (first entry)

DE DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein.

KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytosolic; haemostatic; human; rHA synthase gene; human albumin; HA;
KW DPI-14; DX-890; chimeric.

OS Homo sapiens.

OS Chimeric.

OS Unidentified.

PN US2004171794-A1.

PD 02-SEP-2004.

PF 07-FEB-2003; 2003US-00361997.

PR 07-FEB-2003; 2003US-00361997.

PA (LADN/) LADNER R C.

PA (LEVA/) LEY A C.

PI Ladner RC, Ley AC;

XX MPI: 2004-625120/60.

DR N-PSDB; ADR90019.

PT New Kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.

PS Example 22; SEQ ID NO 45; 123pp; English.

CC The invention relates to proteins comprising Kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytosolic and haemostatic agent. The present sequence is a DPI-14- (GGS) 4
CC GG-rHA- (GGS) 4 GG-DX-890 fusion protein. This fusion protein contains DPI-
CC 14 CDNA encoding protein, GS linker region, rHA (human albumin) synthase
CC gene encoding protein and DX-890 encoding protein. This sequence is used
CC in the exemplification of the invention.

XX Sequence 753 AA;

Query Match 100.0%; Score 329; DB 8; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 698 EACNLPYVGPICIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 753

RESULT 22

AAAR9167
ID AAAR9167 standard; protein; 56 AA.

AC AAAR9167;

DT 12-FEB-1997 (first entry)

XX Genetically engineered aprotinin-like Kunitz domain (EPI-HNE-3).
DE Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX Synthetic.
OS
XX WO9620278-A2.
PN
XX 04-JUL-1996.
PD
XX 15-DEC-1995; 95WO-US016349.
PE
XX 16-DEC-1994; 94US-00358160.
PR
XX (PROT-) PROTEIN ENG CORP.
PA
XX Ley AC, Ladner RC, Guerman SK, Roberts BL, Markland W, Kent RB;
PI WPI; 1996-321851/32.
DR
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX Claim 1; Page 49; 105pp; English.
PS
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR9146-R99211
CC
SQ Sequence 56 AA;
Query Match 98.5%; Score 324; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 6,2e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 ACNLPYVAGPCIAFPFPMWFAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVAGPCIAFPFPMWFAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
RESULT 23
ADF71967
ID ADF71967 standard; protein; 56 AA.
AC ADF71967;
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:47.
DE
XX ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.
XX
XX Homo sapiens.
OS
XX WO2003103475-A2.
PN
XX 18-DEC-2003.
PD
XX 06-JUN-2003; 2003WO-US017665.
PS

XX 07-JUN-2002; 2002US-0387239P.
PR 28-AUG-2002; 2002US-0407003P.
XX (DYAX-) DYAX CORP.
PA
XX Ladner RC, Ley AC, Hiranani S, Williams A;
PI WPI; 2004-062190/06.
DR
XX Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.
XX
XX Disclosure; SEQ ID NO 47; 46pp; English.
PS
XX The present invention describes a method (M1) for preventing or reducing
CC ischaemia in a patient. M1 involves administering to the patient a
CC composition comprising a polypeptide (I) having an amino acid sequence of
CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
CC reducing ischaemia in a patient such as peroperative blood loss due to a
CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
CC is also useful for preventing or reducing the onset of systemic
CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (I) to a patient. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 56 AA;
Query Match 98.5%; Score 324; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 6,2e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 ACNLPYVAGPCIAFPFPMWFAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVAGPCIAFPFPMWFAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
RESULT 24
ADF71968
ID ADF71968 standard; protein; 56 AA.
AC ADF71968;
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:48.
DE
XX ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.
XX
XX Homo sapiens.
OS
XX WO2003103475-A2.
PN
XX 18-DEC-2003.
PD
XX 06-JUN-2003; 2003WO-US017665.
PE
XX 07-JUN-2002; 2002US-0387239P.
PR 28-AUG-2002; 2002US-0407003P.
XX (DYAX-) DYAX CORP.
PA
XX Ladner RC, Ley AC, Hiranani S, Williams A;
PI WPI; 2004-062190/06.
DR
XX Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.
XX
XX Disclosure; SEQ ID NO 48; 46pp; English.
PS

XX The present invention describes a method (M1) for preventing or reducing
 CC ischaemia in a patient. M1 involves administering to the patient a
 CC composition comprising a polypeptide (I) having an amino acid sequence of
 CC ADP1926 and inhibiting kallikrein. (I) has vasotropic activity, and can
 CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
 CC reducing ischaemia in a patient such as peroperative blood loss due to a
 CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
 CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
 CC is also useful for preventing or reducing the onset of systemic
 CC inflammatory response associated with a surgical procedure in a patient
 CC which involves administering (I) to a patient. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 56 AA;

Query Match 98.5%; Score 324; DB 8; Length 56;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACNLPVIRGPCIAPFPFMAFDVAVKGCYLPFYGGCGGNGNKFYSEKECREYCGVP 56
 DB 2 ACNLPVIRGPCIAPFPFMAFDVAVKGCYLPFYGGCGGNGNKFYSEKECREYCGVP 56

RESULT 25

AAR99214
 ID AAR99214 standard; protein; 141 AA.

AC AAR99214;

DT 14-FEB-1997 (first entry)

DE Modified Kunitz domain EPI-HNE-3.

KW Agprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alaph antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.

OS Synthetic.

PN WO9620278-A2.

PD 04-JUL-1996.

PF 15-DEC-1995; 95WO-US016349.

PR 16-DEC-1994; 94US-00358160.

PA (PROT-) PROTEIN ENG CORP.

PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

DR WPI; 1996-321851/32.

DR N-PSDB; AAT35166, AAT35168.

PT New engineered inhibitors of human neutrophil elastase - cong. aprotinin
 PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.

PS Claim 1; Page 68-69; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived Kunitz domains can be used to treat such

CC respiratory disorders. See AAR99146-R99211. Fusion genes were used in the
 CC production of the Kunitz domain derivatives. Protein expression cassettes
 CC are then cloned into the plasmid pHL-D2 using BstBI and EcoRI
 CC restriction sites. The cloned sequence is under the transcriptional
 CC control of Pichia pastoris axol gene promoter and regulatory sequences
 CC and downstream polyadenylation and transcription termination sequences.
 CC Transformed strains of P. pastoris were used to express the various EPI-
 CC HNE proteins derived from the BPTI and ITI-D2 Kunitz domains. This
 CC sequence is a modified Kunitz domain (EPI-HNE-3) which was expressed from
 CC a pHL-D2 plasmid construct designated pHL-D2 (MfalpnapPrePro:EPI-HNE-3)

XX Sequence 141 AA;

Query Match 98.5%; Score 324; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACNLPVIRGPCIAPFPFMAFDVAVKGCYLPFYGGCGGNGNKFYSEKECREYCGVP 56
 DB 87 ACNLPVIRGPCIAPFPFMAFDVAVKGCYLPFYGGCGGNGNKFYSEKECREYCGVP 141

Search completed: February 23, 2005, 03:28:14
 Job time : 75 secs